

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd

OM protein - protein search, using sw model

Run on: December 12, 2003, 14:43:27 ; Search time 52.1387 Seconds
(without alignments)
2036.647 Million cell updates/sec

Title:	PCT-US03-24332-6
Perfect score:	3343

Sequence: 1 MDYKDDDDKLAANXALRG...GDTSGDYKKALLLLCGEDD 669

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

```
Minimum DB seq length: 0
Maximum DB seq length: 20000000000
```

```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
```

Database :
A_Geneseq_15Jun03.*
1: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1980.DAT *
2: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1981.DAT *
3: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1982.DAT *
4: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1983.DAT *
5: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1984.DAT *
6: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1985.DAT *
7: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1986.DAT *
8: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1987.DAT *
9: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1988.DAT *
10: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1989.DAT *
11: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1990.DAT *
12: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1991.DAT *
13: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1992.DAT *
14: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1993.DAT *
15: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1994.DAT *
16: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1995.DAT *
17: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1996.DAT *
18: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1997.DAT *
19: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1998.DAT *
20: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1999.DAT *
21: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT *
22: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT *
23: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT *
24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	3337	99.8	669	24	AB56649	Modified annexin p
2	1708	51.1	766	11	AAK03726	Human placenta-der
3	1706	51.0	672	11	AAK03725	Human placenta-der
4	1688	50.5	675	24	ABU54621	Human NOVX polypep
5	1593	47.7	319	24	AB56648	Human annexin V pr
6	1580	47.3	318	20	AA113925	S65T GFP variant/h
7	1570	47.0	319	15	AA575645	Rat annexin-V. Ra
8	1558	46.6	736	22	AB515948	Novel human diagno
9	1550	45.8	319	20	AA113924	S65T GFP variant/h

1	Mouse ischaemic co	11	1530	45.8	319	23	ABBS7067
2	Annexin V/urokinas	10	1452.5	43.4	600	21	AAV92290
3	CBP-I. Homo sapi	12	1451.5	43.4	319	13	AAAP6276
4	Calmodulin I (Ch	13	1451.5	43.4	319	13	AAAR1071
5	Human CBP-I prote	14	1451.5	43.4	319	23	ABG32550
6	Placental coagulat	15	1451.5	43.4	320	9	AAAP8051
7	Vascular anti-coag	16	1451.5	43.4	320	10	AAAP1953
8	PAP-I. Homo sapi	17	1451.5	43.4	320	12	AAAY3302
9	SETT Gfp variant/H	18	1451.5	43.4	320	20	AAAY3993
10	Amino acid sequenc	19	1451.5	43.4	320	21	AAAY4768
11	Human annexin V, c	20	1451.5	43.4	320	23	AAAG3120
12	anticoagulant PP4	21	1448.5	43.3	320	10	AAAP9053
13	CBP-I isolated fro	22	1447.5	43.3	320	9	AAAP82317
14	CBP-1. Homo sapi	23	1446.5	43.3	319	13	AAAB6180
15	Sequence vascular	24	1445.5	43.2	320	9	AAAP9242
16	Sequence vascular	25	1445.5	43.2	320	9	AAAP9714
17	Vascular anticoagu	26	1445.5	43.2	320	12	AAAR11910
18	Modified human an	27	1442.5	43.1	327	22	AAAB50863
19	Modified human an	28	1442.5	43.1	327	22	AAAB50864
20	Modified human an	29	1442.5	43.1	327	22	AAAB50865
21	Modified human an	30	1441.5	43.1	320	10	AAAP1363
22	Human lipocortin-V	31	1419.5	42.5	319	13	AAAR52718
23	CBP-1. Homo sapi	32			321	20	AAAY3296
24	SETT Gfp variant/H	33	921	27.6	321	23	ABG96729
25	Human ovarian cance	34	921	27.6	321	23	AAAB36617
26	Human cancer associ	35	920	27.5	324	21	AAAB36617
27	Anticoagulative PP	36	920	27.5	321	21	AAAP1963
28	Amino acid sequenc	37	904.5	27.1	320	21	AAAY4790
29	Lung cancer associ	38	897	26.5	208	21	AAAB8393
30	Annexin XI type I	39	871	26.1	503	14	AAAR417
31	Annexin XI type I	40	863	25.8	505	10	AAAR4128
32	Lung cancer associ	41	860	25.7	505	20	AAAY07117
33	Human polypeptide	42	852	25.5	299	23	AAAP6934
34	Sequence vascular	43	852.5	24.6	327	9	AAAP1954
35	Vascular anti-coag	44	852.5	24.6	327	10	AAAR5764
36	VAC-beta. Synthe	45	822.5	24.6	327	22	AAAR7865
37	Human protein SBO						

ALIGNMENTS

XX	RESULT 1
XX	ABP56249
XX	ID ABP56249 standard; Protein; 669 AA.
XX	AC ABP56249;
XX	DT 28-MAR-2003 (first entry)
XX	DE Modified annexin protein SEQ ID NO:6.
XX	KW Annexin; modified; thrombosis; annexin V; thrombolytic;
XX	KW coronary thrombosis; overt cerebral thrombosis; arterial thrombosis
XX	KW transient cerebral ischaemic attack; venous thrombosis.
XX	OS Homo sapiens.
XX	OS Synthetic.
XX	Key Location/Qualifiers
XX	FT Misc-difference 15
XX	FT /label= unknown
XX	FT /note= "encoded by TCN"
XX	FT Misc-difference 374
XX	FT /label= unknown
XX	FT /note= "encoded by NNN"
XX	FT Misc-difference 351
XX	FT /label= unknown
XX	FT /note= "encoded by NNN"
XX	FN WO200267857-A2.
XX	FD 06-SEP-2002.
XX	

PF 21-FEB-2002; 2002WO-US05079.
 XX
 PR 21-FEB-2001; 2001US-270402P.
 PR 21-NOV-2001; 2001US-332582P.
 XX
 PA (SURRE-) SURREMED INC.
 PI Allison A;
 XX
 DR WPI; 2003-123062/12.
 DR N-PSDB; ABZ21926.
 XX
 PT Novel isolated modified annexin proteins comprising annexin protein
 PT coupled to polyethylene glycol or additional proteins, useful for
 PT treating thrombosis e.g. coronary thrombosis and overt cerebral
 PT thrombosis -
 XX
 PS Claim 6; Page 59-62; 62pp; English.
 XX
 CC The present invention describes a modified annexin protein (I) comprising
 CC an annexin protein coupled to: (i) polyethylene glycol (PEG); or (ii) an
 CC additional protein. (II) has thrombolytic activity and can be used as a
 CC thrombosis modulator, and an inhibitor of cellular and humoral
 CC mechanisms by which platelet aggregation is amplified. (I) can be used
 CC for treating a subject at risk from thrombosis. Preferably, a subject
 CC pharmaceutical composition comprising (I) is administered to a subject
 CC after coronary thrombosis, overt cerebral thrombosis, or transient
 CC cerebral ischaemic attack. More preferably, the pharmaceutical
 CC composition is administered to a diabetic patient who is at risk of
 CC arterial thrombosis. The pharmaceutical composition can also be
 CC administered during pregnancy or parturition. (I) is also useful for
 CC treating arterial or venous thrombosis caused by any medical procedure
 CC or condition as described above. (I) prevents arterial or venous
 CC thrombosis without increasing haemorrhage. The present sequence
 CC represents a modified annexin protein from the present invention.
 XX
 SQ Sequence 669 AA;
 Query Match 99.8%; Score 3337; DB 24; Length 669;
 Best Local Similarity 100.0%; Pred. No. 8.9e-241;
 Matches 669; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MDYKDDDDKLAANXALRGVTDPGSGGRADAELRAKMKGLGTDESDILNLTARSA 60
 DB 1 MDYKDDDDKLAANXALRGVTDPGSGGRADAELRAKMKGLGTDESDILNLTARSA 60
 QY 61 QROQIAEEFKTLFGRDLVNDKSELTGKFEKLIVALMKPSRLYDAYELKHAUKGATDEX 120
 DB 61 QROQIAEEFKTLFGRDLVNDKSELTGKFEKLIVALMKPSRLYDAYELKHAUKGATDEX 120
 QY 121 VLTEIIASRTPEELRAIKQAYEEYGSNLEDDVVGDTSGYQMLVLLQANRDPPTAID 180
 DB 121 VLTEIIASRTPEELRAIKQAYEEYGSNLEDDVVGDTSGYQMLVLLQANRDPPTAID 180
 QY 181 DAQVELDAQALFQAGELKMGTDSEKFTIITGRSVSHLRVFDKWTISGFOIEETIDE 240
 DB 181 DAQVELDAQALFQAGELKMGTDSEKFTIITGRSVSHLRVFDKWTISGFOIEETIDE 240
 QY 241 TSGNLENLLAVVSIISIPAYLAETLYAMKAGDHDHLLIVISRSEIDLNFNRKEF 300
 DB 241 TSGNLENLLAVVSIISIPAYLAETLYAMKAGDHDHLLIVISRSEIDLNFNRKEF 300
 QY 301 RKNFATSLYSWIKDTSQDYKKAALLLCGGEDDXRSHSGLEVLFGPGSGTXALRGVTDF 360
 DB 301 RKNFATSLYSWIKDTSQDYKKAALLLCGGEDDXRSHSGLEVLFGPGSGTXALRGVTDF 360
 QY 361 SGFGGRADAELRAKMGGLGTDESDILNLTARSMORQOIAEEFTLGRDLVNDKSE 420
 DB 361 SGFGGRADAELRAKMGGLGTDESDILNLTARSMORQOIAEEFTLGRDLVNDKSE 420
 QY 421 LTGKFEKLIVALMKPSRLYDAYELKHAUKGATDEKLTIIISRTPEELRAIKQAYEE 480
 DB 421 LTGKFEKLIVALMKPSRLYDAYELKHAUKGATDEKLTIIISRTPEELRAIKQAYEE 480

QY 481 YGSNLEDDVVGDTSGYQMLVLLQANRDPPTAIDDAQELFQAGELKMGTDDE 540
 DB 481 YGSNLEDDVVGDTSGYQMLVLLQANRDPPTAIDDAQELFQAGELKMGTDDE 540
 QY 541 KFTIITGRSVSHLRVFDKWTISGFOIEETIDRETSGNLENLLAVVKSIRSIAYLA 600
 DB 541 KFTIITGRSVSHLRVFDKWTISGFOIEETIDRETSGNLENLLAVVKSIRSIAYLA 600
 QY 601 ETLVYAMKAGDHDHLLIVISRSEIDLNFNRKEFRKPFATSLYSMTKQDTSQDYKKA 660
 DB 601 ETLVYAMKAGDHDHLLIVISRSEIDLNFNRKEFRKPFATSLYSMTKQDTSQDYKKA 660
 QY 661 LLLCGEDD 669
 DB 661 LLLCGEDD 669
 RESULT 2
 AAR03726
 ID AAR03726 standard; protein; 786 AA.
 XX
 AC AAR03726;
 XX
 DT 25-MAR-2003 (updated)
 DT 04-JUL-1990 (first entry)
 XX
 DE Human placenta-derived coagulation inhibitor protein.
 XX
 KW Human, placenta; coagulation inhibitor; anticoagulant.
 XX
 OS Homo sapiens.
 XX
 PN EP351826-A.
 XX
 PD 24-JAN-1990.
 XX
 PF 19-JUL-1989; 89EP-0113261.
 XX
 PR 21-JUL-1988; 88JP-0182833.
 XX
 PA (KOMA) KOMA CO LTD.
 XX
 PI Iwasaki A, Suda M, Saino Y;
 XX
 DR WPI; 1990-024228/04.
 DR N-PSDB; AAQ02888.
 XX
 PT Placental coagulation inhibitor polypeptide -
 PT having strong anticoagulation activities and obtained in large
 PT amount by recombinant DNA techniques.
 XX
 PS Disclosure; fig. 5; 24pp; English.
 XX
 CC The polypeptide has properties similar to those of placental
 CC coagulation inhibitor derived from the human placenta. It
 CC can be produced in large amounts and at a low price. It has
 CC strong anticoagulant activities and may be used for the
 CC prevention and treatment of eg thrombosis and DIC
 CC (disseminated intravascular coagulation) in the brain,
 CC heart and peripheral blood vessels such as cerebral and
 CC myocardial infarction. The DNA fragment encoding the CPB-II
 CC polypeptide was obtained from a human placental cDNA library
 CC using a CPB-II specific antibody as a probe. The DNA was
 CC used to prepare a recombinant plasmid which was then used to
 CC transform cells of a microorganism. See also AAR03725, AAQ02887
 CC and AAQ02888.
 CC (Updated on 25-MAR-2003 to correct PA field.)
 XX
 SQ Sequence 786 AA;
 Query Match 51.1%; Score 1708; DB 11; Length 786;
 Best Local Similarity 51.2%; Pred. No. 4.4e-119;

Matches	344;	Conservative	131;	Mismatches	179;	Indels	18;	Gaps	5;
QY	12	AANKALRGTVTDSGFDGRADAEVLKRAKMGLTGDEDSINLLTARSNAORQIAEEFKT	71						
Db	5	AQAKYKRSIHDPFDPNODAEALYTAKKGSGDEALITDIITRSNRQREVCQYKS	64						
QY	72	LFGRDLVNDKMSLTKGFEKLYALMKPSRLDYAVELKAKAGTDEKVTETIASTRP	131						
Db	65	LYGDLIADLKVELTGFEELIVGLMRPAYCDAKEIKOISIGITDEKCLIEIILASTN	124						
QY	132	EEIRAIKQAYEEYGSNLEDDVVGDTSGYQRMVLVLLQANRDPDAIDAQVELDAQAL	191						
Db	125	EQHQVLAAKDAVEEDLEADIGDTSGHQKMLVLLQGTREDDVVSSEDLVQDVQDL	184						
QY	192	FQAGELKMGTDDEKFTITLIGTRSVSHLRVFDKMTISGQIEETIDRETSGNLENLLA	251						
Db	185	YEAGEELKMGDEAQFIILGNRSKQHLRVFEBYELTKTKPEIASIRGELSDFEHLMLA	244						
QY	252	VVKSIRSIIPAYLAETLYAMKAGTDDHTLIRIVSRSEIDLFNIRKEFRKNFATSLYSM	311						
Db	245	VVKCIRSTPEYFAERLFKAMKGLGTRDNTLIRIMVSRSLDVLDRIFRTYKESLYSM	304						
QY	312	IKGDTSGDYKALLLLCGGEDDYRSR--SGLEVLFG--GPGSTXALRGTVTDFSGFD	364						
Db	305	IKNDTSGEYKTKTLKLSGGDDDAQGFPEPAQVAYQWELSAVARVELKGTVPANDFN	364						
QY	365	GRADAEVLKRAKMGLTGDEDSINLLTARSNAORQIAEEFKTIGRDLVNDKMSLTKG	424						
Db	365	PDADAKALKRAKMGLTGDEDTITDIITHSNVQRIQRTFSSHGRDMLDKSEISGD	424						
QY	425	FEKLYALMKPSRLDYAVELKHAKLGADEKVLTEIIASRTPPEELAIKQAYEEYGSN	484						
Db	425	LARLIIGLMPPAHYDAKQKLMKMEGAGDEKALIEILATRNALIRAINEXKYKHYS	484						
QY	485	LEDDVVGDTSGYQRMVLVLLQANRDP---DTAIDAQVELDAQALFQAGELKMGTD-	538						
Db	485	LEBALSDTSGHFRRIILSLATGHRREGGENLDQAREDAQV---AAETLEIADTPSGCKT	541						
QY	539	--BEKFTITLIGTRSVSHLRVFDKMTISGQIEETIDRETSGNLENLLAVKSIIRSI	596						
Db	542	SLERFMFTILCTRSYFHLRRVFEETIKMTNVDEHTIKKEMSGDVDAFVALVQSVKXP	601						
QY	597	AYLAETLYAMKAGTDDHTLIRIVSRSEIDLFNIRKEFRKNFATSLYSMKDTSQDY	656						
Db	602	LFPAADKLKXMKAGTDEKTLIRIMVSRSEIDLIRIRREFIKYKSLHQALEGTSDF	661						
QY	657	KKALLLTCGGED 668							
Db	662	LKALLLTCGGED 673							
RESULT 3									
AAR03725									
ID AAR03725 standard; protein; 672 AA.									
XX									
AC AAR03725;									
XX									
DT 25-MAR-2003 (updated)									
XX									
DT 04-JUL-1990 (first entry)									
XX									
DE Human placenta-derived coagulation inhibitor.									
XX									
KW Human; placenta; coagulation inhibitor; anticoagulant.									
XX									
XX OS Homo sapiens.									
XX									
XX EP51826-A.									
XX									
XX PD 24-JAN-1990.									
XX									
XX PF 19-JUL-1989; 89EP-0113261.									
XX									
PR 21-JUL-1988; 88JP-0182633.									

XX	(KOMA) KOMA CO LTD.
PA	Iwasaki A, Suda M, Saino Y;
PI	WPI, 1990-024228/04.
XX	DR N-P-SDB; AAQ02887.
DR	Placental coagulation inhibitor polypeptide -
PT	amount by recombinant DNA techniques.
PS	Claim 2; page 15, 24pp; English.
XX	The polypeptide has properties similar to those of placental
CC	coagulation inhibitor derived from the human placenta. It
CC	can be produced in large amounts and at a low price. It has
CC	strong anticoagulant activities and may be used for the
CC	prevention and treatment of eg thrombosis and DIC
CC	(disseminated intravascular coagulation) in the brain,
CC	heart and peripheral blood vessels such as cerebral and
CC	myocardial infarction. The DNA fragment encoding the CPB-II
CC	polypeptide was obtained from a human placental cDNA library
CC	using a CPB-II specific antibody as a probe. The DNA was
CC	used to prepare a recombinant plasmid which was then used to
CC	transform cells of a microorganism. See also AAQ02887.
CC	(updated on 25-MAR-2003 to correct PA field.)
XX	Sequence 672 AA;
QQ	Query Match 51.0%; Score 1706; DB 11; Length 672;
QQ	Best Local Similarity 51.0%; Pred. No. 5,1e-119;
QQ	Matches 343; Conservative 132; Mismatches 179; Indels 18; Gaps 5;
QY	12 AANKALRGTVTDSGFDGRADAEVLKRAKMGLTGDEDSINLLTARSNAORQIAEEFKT
Db	4 AQAKYKRSIHDPFDPNODAEALYTAKKGSGDEALITDIITRSNRQREVCQYKS 63
QY	72 LFGRDLVNDKMSLTKGFEKLYALMKPSRLDYAVELKHAKLGADEKVLTEIIASRTP
Db	64 LYGDLIADLKVELTGFEELIVGLMRPAYCDAKEIKOISIGITDEKCLIEIILASTN 123
QY	132 EEIRAIKQAYEEYGSNLEDDVVGDTSGYQRMVLVLLQANRDPDAIDAQVELDAQAL
Db	124 EQHQVLAAKDAVEEDLEADIGDTSGHQKMLVLLQGTREDDVVSSEDLVQDVQDL 183
QY	192 FQAGELKMGTDDEKFTITLIGTRSVSHLRVFDKMTISGQIEETIDRETSGNLENLLA
Db	184 YENGELKMGTDDEAQFIILGNRSKQHLRVFEBYELTKTKPEIASIRGELSDFEHLMLA 243
QY	252 VVKSIRSIIPAYLAETLYAMKAGTDDHTLIRIVSRSEIDLFNIRKEFRKNFATSLYSM
Db	244 VVKCIRSTPEYFAERLFKAMKGLGTRDNTLIRIMVSRSLDVLDRIFRTYKESLYSM 303
QY	312 IKGDTSGDYKALLLLCGGEDDYRSR--SGLEVLFG--GPGSTXALRGTVTDFSGFD
Db	304 IKNDTSGEYKTKTLKLSGGDDDAQGFPEPAQVAYQWELSAVARVELKGTVPANDFN 363
QY	365 GRADAEVLKRAKMGLTGDEDSINLLTARSNAORQIAEEFKTIGRDLVNDKMSLTKG
Db	364 PDADAKALKRAKMGLTGDEDTITDIITRSNVQRIQRTKSHFGDMLDKSEISGD 423
QY	425 FEKLYALMKPSRLDYAVELKHAKLGADEKVLTEIIASRTPPEELAIKQAYEEYGSN
Db	424 LARLIIGLMPPAHYDAKQKLMKMEGAGDEKALIEILATRNALIRAINEXKYKHYS 483
QY	485 LEDDVVGDTSGYQRMVLVLLQANRDP---DTAIDAQVELDAQALFQAGELKMGTD-
Db	484 LEDBALSDTSGHFRRIILSLATGHRREGGENLDQAREDAQV---AAETLEIADTPSGDKT 540
QY	539 --BEKFTITLIGTRSVSHLRVFDKMTISGQIEETIDRETSGNLENLLAVKSIIRSI
Db	541 SLERFMFTILCTRSYFHLRRVFEETIKMTNVDEHTIKKEMSGDVDAFVALVQSVKXP 600

QY 477 YEEYGSNLEDDVVGDTSGYQRMVLLQANRDP-----DTAIDQAVELDAQALFQAG 531
 Db 485 YKEDYKSLDSDALSSDTSGHFRLILSLATGHHESGEVLDPAREDAEIAAT---PSG 540
 QY 532 ELKMGTDSEKFTITLIGTSVSHLRVFPKXMTISGFQIETIDRETSGNLENLLAVYKS 591
 Db 541 DKT--SIETRFMTILCTRSPHLRVFQEFIKMTNVDEHTIKKMSGDVRAFAVAVQS 598
 QY 592 IRSIPAYLAETLYAMKAGTDDHTLIRVIVSRSEIDLFNIRKEFRKNFATSLYSMTKGD 651
 Db 599 VKNPFLEFADKLKYSKMGAGTDEKTLTRIMVSHSIDLIRREFIEKDXSLHQALEGD 658
 QY 652 TSGDYKALLLLCGGED 668
 Db 659 TSGDFLKALLALCGGED 675

RESULT 5
 ID ABP56248 standard; Protein; 319 AA.
 XX AC ABP56248;
 XX 28-MAR-2003 (first entry)
 XX DE Human annexin V protein SEQ ID NO:3.
 XX KW Annexin; modified; thrombosis; annexin V; thrombolytic;
 KW coronary thrombosis; overt cerebral thrombosis; arterial thrombosis;
 KW transient cerebral ischaemic attack; venous thrombosis.
 XX OS Homo sapiens.
 XX PN W0200267857-A2.
 XX PD 06-SEP-2002.
 XX PF 21-FEB-2002; 2002MO-US05079.
 XX PR 21-FEB-2001; 2001US-270402P.
 XX PR 21-NOV-2001; 2001US-332582P.
 XX PA (SUR-) SURROMED INC.
 XX PI Allison A;
 XX PT WPI; 2003-129062/12.
 DR N-PSDB; ABZ21925.
 XX Novel isolated modified annexin proteins comprising annexin protein
 PT coupled to polyethylene glycol or additional proteins, useful for
 PT treating thrombosis e.g. coronary thrombosis and overt cerebral
 PT thrombosis -
 PS Claim 6; Page 36; 62pp; English.

The present invention describes a modified annexin protein (I) comprising
 an annexin protein coupled to: (i) polyethylene glycol (PEG); or (ii) an
 additional protein. (I) has thrombolytic activity and can be used as a
 thrombosis modulator, and an inhibitor of cellular and humoral
 mechanisms by which platelet aggregation is amplified. (I) can be used
 for treating a subject at risk from thrombosis. Preferably, a
 pharmaceutical composition comprising (I) is administered to a subject
 after coronary thrombosis, overt cerebral thrombosis, or transient
 cerebral ischaemic attack. More preferably, the pharmaceutical
 composition is administered to a diabetic patient who is at risk of
 arterial thrombosis. The pharmaceutical composition can also be
 administered during pregnancy or parturition. (I) is also useful for
 treating arterial or venous thrombosis caused by any medical procedure
 or condition as described above. (I) prevents arterial or venous
 thrombosis without increasing haemorrhage. The present sequence
 represents human annexin V, which is used in an example from the
 present invention.

XX SQ Sequence 319 AA;
 Query Match 47.7%; Score 1593; DB 24; Length 319;
 Best Local Similarity 100.0%; Pred. No. 5.5e-111;
 Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 AIRGVTDSGFGDADAEVLRKAMKGLGTEDSLINLLTRSNAAQQAEEFKTLFGR 75
 Db 2 AIRGVTDSGFGDADAEVLRKAMKGLGTEDSLINLLTRSNAAQQAEEFKTLFGR 61
 QY 76 DLVNDKSELTGFEKFLIVALKMPSRLYDAVELKHAKLGAQTDKVLTEIIASRPELR 135
 Db 62 DLVNDKSELTGFEKFLIVALKMPSRLYDAVELKHAKLGAQTDKVLTEIIASRPELR 121
 QY 136 AIKQAYEEYGSNLEDDVVGDTSGYQRMVLLQANRDPDTAIDDAQVELDAQALFQAG 195
 Db 122 AIKQAYEEYGSNLEDDVVGDTSGYQRMVLLQANRDPDTAIDDAQVELDAQALFQAG 181
 QY 196 ELKMGTDSEKFTITLIGTSVSHLRVFPKXMTISGFQIETIDRETSGNLENLLAVYKS 255
 Db 182 ELKMGTDSEKFTITLIGTSVSHLRVFPKXMTISGFQIETIDRETSGNLENLLAVYKS 241
 QY 236 IRSIPAYLAETLYAMKAGTDDHTLIRVIVSRSEIDLFNIRKEFRKNFATSLYSMTKGD 315
 Db 242 IRSIPAYLAETLYAMKAGTDDHTLIRVIVSRSEIDLFNIRKEFRKNFATSLYSMTKGD 301
 QY 316 TSGDYKALLLLCGGED 333
 Db 302 TSGDFLKALLALCGGED 319

RESULT 6
 ID AAY13925 standard; Protein; 318 AA.
 XX AC AAY13925;
 XX DT 13-JUL-1999 (first entry)
 XX DE S65T GFP variant/Annexin V protein.
 KW GFP; green fluorescent protein; annexin; fusion protein; apoptosis;
 KW fluorescent intensity; anionic phospholipid binding affinity;
 KW asymmetric distribution; plasma membrane phospholipid;
 KW apoptotic cell detection.
 XX OS Aequorea victoria.
 OS Homo sapiens.
 OS Synthetic.
 XX PN W09919470-A2.
 XX PD 22-APR-1999.
 XX PF 09-OCT-1998; 98WO-US21444.
 XX PR 09-OCT-1997; 97US-0948276.
 XX PA (REGC) UNIV CALIFORNIA.
 XX PI Ernst JD;
 XX DR WPI; 1999-277634/23.
 XX Bifunctional fusion protein useful for the detection of apoptotic
 PT cells
 PS Claim 2; Page 17-18; 23pp; English.

This sequence represents an example of a protein of the invention.
 CC The proteins are bifunctional Aequorea victoria green fluorescent protein
 CC (GFP)-annexin fusion proteins, where the GFP and annexin moieties provide

CC greater or equal fluorescent intensity and anionic phospholipid binding
 CC affinity, respectively, than do the corresponding unfused GFP and annexin
 CC proteins. An early manifestation of apoptosis is the loss of the
 CC asymmetric distribution of plasma membrane phospholipids, which results
 CC in exposure of anionic phospholipids on the extracellular leaflet of the
 CC plasma membrane. The GFP-annexin V fusion proteins are used for the
 CC detection of apoptotic cells by flow cytometry or fluorescent microscopy.
 CC The fusion proteins provide for homogeneously labelled annexin, with
 CC fluorescence properties that do not change upon binding membrane
 CC phospholipids, unlike prior art FITC-labelled annexins, where quenching
 CC of FITC-annexin V fluorescence by 40-50% occurs upon binding phospholipid
 CC membranes.

XX Sequence 318 AA;

Query Match 47.3%; Score 1580; DB 20; Length 318;
 Best Local Similarity 99.4%; Pred. No. 5.1e-110;
 Matches 316; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 16 ALRGTVDFSGFGRADAEVLRKAMKGLGTDEDSINLITARSNAQRQIAEEFTLFG 75
 DB 1 ALRGTVDFSGFGRADAEVLRKAMKGLGTDEDSINLITARSNAQRQIAEEFTLFG 60
 QY 76 DLVNDKSELTKGFEKLIYALMKPSRLYDAVELKAKLAGTDEKVLTEIISRTPELR 135
 DB 61 DLVNDKSELTKGFEKLIYALMKPSRLYDAVELKAKLAGTDEKVLTEIISRTPELR 120
 QY 136 AIKQAEERYGSLNEDDVGDTSGYQRMVLVLLQANRDPDTAIDDAQVELDAQALFQAG 195
 DB 121 AIKQAEERYGSLNEDDVGDTSGYQRMVLVLLQANRDPDTAIDDAQVELDAQALFQAG 180
 QY 196 ELKMGTEDEKFTITLGRSVSHLRVPKMTISGQIETIDRETSNLENLLAVYKS 255
 DB 181 ELKMGTEDEKFTITLGRSVSHLRVPKMTISGQIETIDRETSNLENLLAVYKS 240
 QY 256 IRSIPAYLAETLYYAMKAGTDDHTLIRIVSRSEIDLFNIRKEFRKNFATSLYSMIKGD 315
 DB 241 IRSIPAYLAETLYYAMKAGTDDHTLIRIVSRSEIDLFNIRKEFRKNFATSLYSMIKGD 300
 QY 316 TSGDYKKALLLLCGGEDD 333
 DB 301 TSGDYKKALLLLCGGEDD 318

RESULT 7

AAR75695
 ID AAR75695 standard; peptide; 319 AA.

XX AAR75695;

DT 21-JAN-1996 (first entry)

XX Rat annexin-V.

KM Amyloid precursor protein; APP; annexin-V; Alzheimer's disease;
 disease diagnosis; therapy; antibody.

XX Rattus rattus.

XX Key Location/Qualifiers

FT Peptide 57..68

FT Peptide 85..95

FT Peptide 107..120

FT Peptide 259..284

PN EP655626-A1.

PD 31-MAY-1995.

PF 10-NOV-1994; 94EP-0308303.

PR 23-AUG-2000; 2000US-0649167.

XX 10-NOV-1993; 93US-0149975.

PA (MCLE-) MCLEAN HOSPITAL CORP.

PI Honda T, Nixon R;

XX WPI; 1995-195688/26.

PT New peptide(s) associated with Alzheimer's disease - namely p33 and
 the amyloid precursor C2 fragment, useful for the prodn. of
 diagnostic antibodies

XX Disclosure; Fig.9; 32pp; English.

PS This amino acid sequence is contained within the 33 kDa protein
 (p33) sequence and the indicated peptides are produced following
 lysyl-endopeptidase cleavage of p33. Detection and quantification
 of this protein is therefore useful for diagnosing the disease.

XX Sequence 319 AA;

Query Match 47.0%; Score 1570; DB 16; Length 319;
 Best Local Similarity 98.7%; Pred. No. 2.9e-109;
 Matches 314; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 16 ALRGTVDFSGFGRADAEVLRKAMKGLGTDEDSINLITARSNAQRQIAEEFTLFG 75
 DB 2 ALRGTVDFSGFGRADAEVLRKAMKGLGTDEDSINLITARSNAQRQIAEEFTLFG 61
 QY 76 DLVNDKSELTKGFEKLIYALMKPSRLYDAVELKAKLAGTDEKVLTEIISRTPELR 135
 DB 62 DLVNDKSELTKGFEKLIYALMKPSRLYDAVELKAKLAGTDEKVLTEIISRTPELR 121
 QY 136 AIKQAEERYGSLNEDDVGDTSGYQRMVLVLLQANRDPDTAIDDAQVELDAQALFQAG 195
 DB 122 AIKQAEERYGSLNEDDVGDTSGYQRMVLVLLQANRDPDTAIDDAQVELDAQALFQAG 181
 QY 196 ELKMGTEDEKFTITLGRSVSHLRVPKMTISGQIETIDRETSNLENLLAVYKS 255
 DB 182 ELKMGTEDEKFTITLGRSVSHLRVPKMTISGQIETIDRETSNLENLLAVYKS 241
 QY 256 IRSIPAYLAETLYYAMKAGTDDHTLIRIVSRSEIDLFNIRKEFRKNFATSLYSMIKGD 315
 DB 242 IRSIPAYLAETLYYAMKAGTDDHTLIRIVSRSEIDLFNIRKEFRKNFATSLYSMIKGD 301
 QY 316 TSGDYKKALLLLCGGEDD 333
 DB 302 TSGDYKKALLLLCGGEDD 319

RESULT 8

ABG19948
 ID ABG19948 standard; Protein; 736 AA.

XX ABG19948;

DT 18-FEB-2002 (first entry)

XX Novel human diagnostic protein #19939.

KM Human; chromosome mapping; gene therapy; forensic;
 food supplement; medical imaging; diagnostic; genetic disorder.

XX Homo sapiens.

PN WO200175067-A2.

PD 11-OCT-2001.

PF 30-MAR-2001; 2001WO-US08631.

PR 31-MAR-2000; 2000US-0540217.

PR 23-AUG-2000; 2000US-0649167.

PA (HYSE-) HYSEQ INC.

XX Drmanac RT, Liu C, Tang YT;
 XX WPI, 2001-639362/73.
 DR N-PSDB; AAS84135.
 XX New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -
 XX Claim 20; SEQ ID No 50307; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences (I) is useful as hybridization probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations,
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG0010-ABG0377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 736 AA;

Query Match 46.6%; Score 1558; DB 22; Length 736;
 Best Local Similarity 49.4%; Pred. No. 6,4e-108;
 Matches 331; Conservative 127; Mismatches 188; Indels 24; Gaps 11;

QY 18 RGVTPDPSGPDGADAEVLRKAMKGLGDESDSILNLTPASNAQOQAEFKTLFGRDL 77
 Db 70 RGSIDHPGPDQDEALYTKMGSGSKKALDITTSFNROQEGCHSKYKSLYKDL 129
 QY 78 VDMKSELTKKEKELVALMKPSRLYDAVELKAKLGAGTDEKVTETIASRTPEEL-RA 136
 Db 130 IADLKVELTGKFERLIVLRMRBPAYCDKAEIKDAISGIGTEKCEIETIASRTNEQHQL 169
 QY 137 IKQAYEEYGSNLEDVVDGTSYIQRMVLVLLQANRDPDAIDQVELDQALFQAGE 196
 Db 190 VKRITMPTFRDLDAIIGDTSGHQKLVLLQGTREDDVVSDDLVQDVLVEAGE 249
 QY 197 LKMGDEKEFTITLGRSVSHLRVFDKMTYSGQIETIDRETSGLKELLAAVKS 256
 Db 250 LKMGDEAGPIYILGRSKQHLIVFDEVLTKTGFIASIRGELSGDFELMLAAVKCI 309
 QY 257 RSPAYLAETLYAMKAGTDDHTLIRIVVSSSEIDLFNIRKFRKNA-TSLYSK-IGK 314
 Db 310 RSTPEYFAERLFRAMKGLGTRDNTLIRIVVSSSEIDMLDIEIFPTKXKESLSMIDKN 369
 QY 315 DTSG-DYKCALLLTCGDEDDXRSR---SGLEVLFO---GGSTYALRGVTIDPSGPDGR 366
 Db 370 DTSGGSKYKTLTKLTSGGDDADQFPRAQYAYQWMLSAVARELKGITVRANDNPD 429
 QY 367 ADAEVLKAMKGLGDESDSILNLTPASNAQOQAEFKTLFGRDLVDMKSELTKGFE 426
 Db 430 ADAKALRKAMKGLGDESDSILNLTPASNAQOQAEFKTLFGRDLVDMKSELTKGFE 426
 QY 427 KLIVALMKPSRLYDAVELKAKLGAGTDEKVTETIASRTPEELRAIKQAYEEYGSNLE 466
 Db 490 RLITGLMPPPAHYDAKOLRKAMEGAGTDEKALIEILATRTNAEIRAINAEAYKEDYHKSLE 549

QY 487 DDVVDGTSYQYRMVLVLLQANRDP-----DTAIDQVELDQALFQAGELKMGTD--- 538
 Db 550 DALSDSTSGHRRRLISLATGCHREGGENIDQANEDQV---AAEILIEIDPTSGKTSI 606
 QY 539 EKEFTITLGRSVSHLRVFDKMTYSGQIETIDRETSGLKELLAAVKSIRISIPAY 598
 Db 607 EIRFMITLCTSHYHVRVIOEFTRLNIVDVEHITKEMSGDIRDAFVAIVGAKTKPLF 666
 QY 599 LAETLYAMKAGTDDHTLIRIVVSSSEIDLFNIRKEFR-KNPAISLYSNIKG-DTSGDY 656
 Db 667 FPDKLYKSMKAGTDEKTLTRIVVSSSEIDMLNIRGIPREKDKSIHQVIXGXTTQGF 726
 QY 657 KXALLLTCGG 666
 Db 727 LKALRALCGG 736

RESULT 9
 ID AAY13924 standard; protein; 319 AA.
 XX AAY13924;
 AC AAY13924;
 XX 13-JUL-1999 (first entry)
 DT 13-JUL-1999 (first entry)
 XX 565T GFP variant/hAnnexin V protein.
 DE GFP, green fluorescent protein; annexin; fusion protein; apoptosis;
 KW fluorescent intensity; anionic phospholipid binding affinity;
 KW asymmetric distribution; plasma membrane phospholipid;
 KM apoptotic cell detection.
 XX Aequorea victoria.
 OS Homo sapiens.
 OS Synthetic.
 PN WO9919470-A2.
 XX 22-APR-1999.
 PD 09-OCT-1998; 98WO-US21444.
 PF 09-OCT-1997; 97US-0948276.
 PR (REGC) UNIV CALIFORNIA.
 XX PA
 XX Ernst JD;
 DR WPI, 1999-277634/23.
 XX Bifunctional fusion protein useful for the detection of apoptotic
 PT cells
 PT Claim 2; Page 15-17; 23pp; English.
 PS This sequence represents an example of a protein of the invention.
 CC The proteins are bifunctional Aequorea victoria green fluorescent protein
 CC (GFP)-annexin fusion proteins, where the GFP and annexin moieties provide
 CC greater or equal fluorescent intensity and anionic phospholipid binding
 CC affinity, respectively, than do the corresponding unfused GFP and annexin
 CC proteins. An early manifestation of apoptosis is the loss of the
 CC asymmetric distribution of plasma membrane phospholipids, which results
 CC in exposure of anionic phospholipids on the extracellular leaflet of the
 CC plasma membrane. The GFP-annexin V fusion proteins are used for the
 CC detection of apoptotic cells by flow cytometry or fluorescent microscopy.
 CC The fusion proteins provide for homogeneously labelled annexin, with
 CC fluorescence properties that do not change upon binding membrane
 CC phospholipids, unlike prior art FITC-labelled annexins, where quenching
 CC of FITC-annexin V fluorescence by 40-50% occurs upon binding phospholipid
 CC membranes.
 CC Sequence 319 AA;

Query Match	45.8%	Score 1530	DB 20	Length 319
Best Local Similarity	95.3%	Pred. No. 2,8e-106		
Matches 303	Conservative 7	Mismatches 8	Indels 0	Gaps 0
QY	16	ALRGTVDFSGFGADAEVLKRAKKGIGTDEDSILNLTARSNAORQIAEFKTLFGR	75	
Db	2	ATRGTVDFSGFGADAEVLKRAKKGIGTDEDSILNLTARSNAORQIAEFKTLFGR	61	
QY	76	DIYVDMKSELTGFEFLIYALMKPSRLIDAYELKAKLGAGTDEKVTETIISRTPEELR	135	
Db	62	DIYVDMKSELTGFEFLIYAMMKPSRLIDAYELKAKLGAGTDEKVTETIISRTPEELS	121	
QY	136	AIKQAYEEBYGSNLIEDVVGDTSGYQGNLVTLLQANRDPITADIAQVLYDAQALFQAG	195	
Db	122	AIKQAYEEBYGSNLIEDVVGDTSGYQGNLVTLLQANRDPITADIAQVLYDAQALFQAG	181	
QY	196	ELKMGIDDEKFTIILCTRSVSHLRVDFPKYMTISGQIIEETIDETSIGNLEMLLAVVKS	255	
Db	182	ELKMGIDDEKFTIIFGTRSVSHLRVDFPKYMTISGQIIEETIDETSIGNLEMLLAVVKS	241	
QY	256	IRSIPIYALETLYYAKKAGCTDHTLIIVYSRSIDLFNIRKFRFNKFTSIYSYIKGD	315	
Db	242	IRSIPIYALETLYYAKKAGCTDHTLIIVYSRSIDLFNIRKFRFNKFTSIYSYIKGD	301	
QY	316	TSGDYKXALLLLCGGEDD 333		
Db	302	TSGDYKXALLLLCGGEDD 319		
RESULT 10				
ABB57067				
ID	ABB57067	standard; Protein; 319 AA.		
AC	ABB57067;			
XX				
DT	07-MAR-2002	(first entry)		
XX				
DE	Mouse ischaemic condition related protein sequence SEQ ID NO:136.			
XX				
KW	Mouse; Ischaemia; compressive ischaemia; occlusive ischaemia;			
XX	vasospastic ischaemia; ischaemic condition; ischaemic disease.			
OS	Mus musculus.			
XX				
PN	WO200189188-A2.			
XX				
PD	22-NOV-2001.			
XX				
PF	18-MAY-2001; 2001WO-JP04192.			
XX				
PR	18-MAY-2000; 2000JP-0145977.			
XX				
PA	(UNIV-) UNIV NIHON SCHOOL JURIDICAL PERSON.			
PI	Ishikawa K, Arai S, Takahashi Y, Nagata T, Ishii Y;			
XX				
DR	WPI: 2002-034733/04.			
XX				
DR	N-PSDB; ABI95289.			
XX				
PS	Claim 2; Page 419-421; 2690pp; English.			
XX				
CC	The present invention describes a method for examining ischaemic			
XX	conditions, comprising measuring the expression levels of particular			
CC	genes (I) in a test sample or determining the expression profile of a			
XX	gene group in the sample comprising genes selected from (I). The method			
CC	is useful for examining the ischaemic condition (e.g. compressive			
XX	ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring			
CC	expression levels of particular genes (ABI99202 to ABI99912, encoding			

Query Match	45.8%	Score 1530;	DB 23;	Length 319;
Best Local Similarity	95.3%;	Pred. No. 2.8e-106;		
Matches 303;	Conservative 7;	Mismatches 8;	Indels 0;	Gaps 0
16	ALNGVTDFSGFPGGRDAEVAEKAKKGGTDEDSITLNLTRASNQAPQIAEERTKTLFGR	75		
2	ATNGVTDFPGFGRDAEVAELKAKKGLGTDEDSITLNLTRSNQGEIAQERTLFGFGR	61		
76	DLVNDKMSLTGFEKELIVALKMPSRLYDAVELKAKLGAQDEKVLTEIIASRTPEELR	135		
62	DLVNDLKSLELTGFEKELIVALKMPSRLYDAVELKAKLGAQDEKVLTEIIASRTPEELS	121		
136	ALIQAYEEERGSNLEDDVGTSGIYQRMVTVLLQANFDPOTAIDDAQVELDAQALFQAG	195		
122	ALIQAYEEERGSNLEDDVGTSGIYQRMVTVLLQANFDPOTAIDDAQVELDAQALFQAG	183		
196	ELKMGDEDEKFTILGTRSVSHLRVFPDKMTISGFOIEITDETSNGENLLAVVKS	255		
182	ELKMGDEDEKFTILGTRSVSHLRVFPDKMTISGFOIEITDETSNGENLLAVVKS	241		
256	IRSIPIAYLAETLYVANKAGATDHTLIRIVRSRSEIDLFNIRKSRKNFATSLYSMTKGD	315		
242	IRSIPIAYLAETLYVANKAGATDHTLIRIVRSRSEIDLFNIRKSRKNFATSLYSMTKGD	301		
316	TSGDYKKALLLCGGEDD	333		
302	TSGDYKKALLLCGGEDD	319		

RESULT 11
AA92930
ID AA92930 standard; Protein; 600 AA.
AC AA92930;
XX 25-OCT-2000 (first entry)
XX Annexin V/uropkinase fusion protein.
XX Annexin V; thrombocyte; carrier; thrombus; thrombolytic; fusion protein;
XX uropkinase; insect cell; fibrinolytic.
XX Unidentified.
XX CN1247195-A.
XX 15-MAR-2000.
XX 12-MAR-1999; 99CN-0113524.
XX 12-MAR-1999; 99CN-0113524.
XX (SHAN-) SHANGHAI INST BIOCHEMISTRY CHINESE ACAD.
XX Wu X, Sun J, Yang G;
XX WPI; 2000-413098/36.
XX N-PSDB; AAA11241.
XX New thrombolytic fusion protein for targeting thrombus - comprises
XX fusion of Annexin V and uropkinase
XX Claim 2; Page 2-4; 20pp; Chinese.

XX CC Annexin V, which has high affinity for active thrombocytes, is used
 CC as a carrier molecule to build a thrombus-targeting thrombolytic fusion
 CC protein. The protein (this sequence) is the result of expression of a
 CC fusion gene comprising the Annexin V gene and a low-molecular urokinase
 CC gene, in insect cells. The Annexin V-scu-PA-32 fusion protein, expressed
 CC in insect cell strain Tn-531-4, has high affinity for active thrombocytes
 CC and has the fibrinolytic activity of urokinase.

XX Sequence 600 AA;

Query Match 43.4%; Score 1452.5; DB 21; Length 600;
 Best Local Similarity 87.3%; Pred. No. 3.7e-100;
 Matches 290; Conservative 18; Mismatches 23; Indels 1; Gaps 1;

QY 2 DYVDDDDKLAAMAKALRGVTFDPSGPDADAEVRKAMKGLGTDDESLINLLTARSNAQ 61
 DB 270 DFEIPEEYEVNAQVLRGTLTDPFGFDEADAEFLRKAMKGLGTDDESLITLLTARSNAQ 329
 QY 62 RQIAIEEFKTLFGRLDVMNKSSELTKGFEKLIVALKMPSRLYDAYELKHAFLGAGTDEKV 121
 DB 330 RQISAFKTLFGRLDLDLKKSELTKGFEKLIVALKMPSRLYDAYELKHAFLGAGTDEKV 389
 QY 122 LTFIISRTPEELRAIKQAYEEYGSNLEDVVGDTSGYQRMVLLQANRDPDAID 181
 DB 390 LTFIISRTPEELRAIKQAYEEYGSNLEDVVGDTSGYQRMVLLQANRDPDAID 449
 QY 182 AQVELDAQALFOAGELKMGTDDEKFTILGTRSVSHLRVFPDKMTTSGFOIEETIDRET 241
 DB 450 AQVELDAQALFOAGELKMGTDDEKFTILGTRSVSHLRVFPDKMTTSGFOIEETIDRET 509
 QY 242 SGNLENLLAVVKSIRSIAPYLAETLYYAMKAGTDDTLIRVYSRSEIDLFINRKEFR 301
 DB 510 SGNLEQLLAVVKSIRSIAPYLAETLYYAMKAGTDDTLIRVYSRSEIDLFINRKEFR 569
 QY 302 KNPATSLYSMIKDTSGDYKALLLCCGEDD 333
 DB 570 KNPATSLYSMIKDTSGDYKALLLCCGEDD 600

RESULT 12

AAR26276 standard; protein, 319 AA.

XX AC AAR26276;
 XX DT 10-MAR-2003 (updated)
 XX DT 04-FEB-1993 (first entry)
 XX DE CPB-I.
 XX KW CPB-I; stabilisation; frozen; molten; processed; activity.
 XX OS Homo sapiens.
 XX PN JP04198195-A.
 XX PD 17-JUL-1992.
 XX PF 28-NOV-1990; 90JP-0328286.
 XX PR 28-NOV-1990; 90JP-0328286.
 XX PA (KAGA) KAGAKU OYOBI KESSEI RYOHO.
 XX PA (KOMA) KOMA CO LTD.
 XX DR WPI; 1992-288937/35.
 XX PT Stabilisation of CPB-I for drug compsn. - by adding basic
 XX PT aminoacid selected from lysine, arginine and/or ornithine
 XX PS Disclosure; Page 2, 4pp; Japanese.

CC CC The sequence given is the amino acid sequence of CPB-I. CPB-I was
 CC used within a method which involved adding basic amino acids to it
 CC which resulted in its stabilisation. This lead to the production of
 CC CPB-I which keeps its activity when it is frozen, molten or has been
 CC processed by several procedures.
 CC (updated on 10-MAR-2003 to add missing OS field.)

XX Sequence 319 AA;

Query Match 43.4%; Score 1451.5; DB 13; Length 319;
 Best Local Similarity 91.5%; Pred. No. 2e-100;
 Matches 290; Conservative 12; Mismatches 14; Indels 1; Gaps 1;

QY 17 LRGITDPSGPDADAEVRKAMKGLGTDDESLINLLTARSNAQRLAEKTLFGRLD 76
 DB 4 LRGITDPSGPDADAEVRKAMKGLGTDDESLITLLTARSNAQRLAEKTLFGRLD 63
 QY 77 LVNDKSELTKFEKLIVALKMPSRLYDAYELKHAFLGAGTDEKVLTEIISRTPEELRA 136
 DB 64 LLDLKSLLTKFEKLIVALKMPSRLYDAYELKHAFLGAGTDEKVLTEIISRTPEELRA 123
 QY 137 IKQAYEEYGSNLEDVVGDTSGYQRMVLLQANRDPDAIDAQVELDAQALFOAGB 196
 DB 124 IKQAYEEYGSNLEDVVGDTSGYQRMVLLQANRDPDAIDAQVELDAQALFOAGB 183
 QY 197 LKMGTDDEKFTILGTRSVSHLRVFPDKMTTSGFOIEETIDRETSGNLENLLAVVKS 256
 DB 184 LKMGTDDEKFTILGTRSVSHLRVFPDKMTTSGFOIEETIDRETSGNLENLLAVVKS 243
 QY 257 RSIAPYLAETLYYAMKAGTDDTLIRVYSRSEIDLFINRKEFRKNPATSLYSMIKDT 316
 DB 244 RSIAPYLAETLYYAMKAGTDDTLIRVYSRSEIDLFINRKEFRKNPATSLYSMIKDT 303
 QY 317 SGNLEQLLAVVKSIRSIAPYLAETLYYAMKAGTDDTLIRVYSRSEIDLFINRKEFR 333
 DB 304 SGNLEQLLAVVKSIRSIAPYLAETLYYAMKAGTDDTLIRVYSRSEIDLFINRKEFR 319

RESULT 13

AAR41021 standard; protein, 319 AA.

XX AC AAR41021;
 XX DT 29-MAR-1994 (first entry)
 XX DE Calphobindin I (CPB-I).
 XX KW Calphobindin I; CPB-I; Protein kinase C; PKC; inhibition; tumour.
 XX OS Homo sapiens.
 XX PN JP05213769-A.
 XX PD 24-AUG-1993.
 XX PF 04-FEB-1992; 92JP-0019032.
 XX PR 04-FEB-1992; 92JP-0019032.
 XX PA (KOMA) KOMA CO LTD.
 XX PA (KAGA-) ZH KAGAKU OYOBI KESSEN RYOHO KENKYUSHO.
 XX DR WPI; 1993-299558/38.
 XX PT Protein kinase C inhibitor effective against malignant tumours -
 XX PT contg. (opt. recombinant) calphobindin I
 XX PS Claim 1; Page 2-3; 6pp; Japanese.
 CC Calphobindin I (CPB-I) or recombinant calphobindin I (r-CPB-I)
 CC inhibits protein kinase C (PKC) and is useful in the treatment of
 CC malignant tumours caused by abnormal activation of PKC. CPB-I is

CC extracted from human or animal organs and may be applied
 CC intravenously, orally, intramuscularly, percutaneously or rectally.
 XX
 SQ Sequence 319 AA;

Query Match 43.4%; Score 1451.5; DB 14; Length 319;
 Best Local Similarity 91.5%; Pred. No. 2e-100;
 Matches 290; Conservative 12; Mismatches 14; Indels 1; Gaps 1;

QY 17 LRGTVDPSGFGDADAEVLKAMKGLGDEDSILNLTIRSNAGROQIAEERKTLFGRD 76
 DB 4 LRGTVDPSGFGDADAEVLKAMKGLGDEDSILNLTIRSNAGROQIAEERKTLFGRD 63
 QY 77 LVNDKSELTGKFEKTLVAMKPSRLYDAVELKAKLGAQDEKVTETIISRPEELRA 136
 DB 64 LDDDKSELTGKFEKTLVAMKPSRLYDAVELKAKLGAQDEKVTETIISRPEELRA 123
 QY 137 IKQAYEEYGSNLEDDVVGDTSGYQRMVLVLLQANRDPDAIDDAQVELDAQALFQAGE 196
 DB 124 IKQAYEEYGSNLEDDVVGDTSGYQRMVLVLLQANRDPDAIDDAQVELDAQALFQAGE 183
 QY 197 LKMGTEBEKFTITIGTSVSHLRVPDKYMTISGFOIETIDRETSGNLEQLLAVKSI 256
 DB 184 LKMGTEBEKFTITIGTSVSHLRVPDKYMTISGFOIETIDRETSGNLEQLLAVKSI 243
 QY 257 RSIPAYLAETLYYAMKAGTDHDTLIRVIVSRSEIDLEFNIRKFRKPFATSLYSMTKGD 316
 DB 244 RSIPAYLAETLYYAMKAGTDHDTLIRVIVSRSEIDLEFNIRKFRKPFATSLYSMTKGD 303
 QY 317 SGDYKRALLLCGGDD 333
 DB 304 SGDYKRALLLCGGDD 319

RESULT 14
 ABG32550
 ID ABG32550 standard; protein; 319 AA.

XX AC ABG32550;
 XX DT 29-NOV-2002 (first entry)
 XX DE Human CPB-1 protein.
 XX KW Human; CPB-1; eye drop; ophthalmological; anexin V; corneal disease;
 XX KW calcium/phospholipid binding protein; polyhydric alcohol.
 XX OS Homo sapiens.
 XX PN WO200267977-A1.
 XX PD 06-SEP-2002.
 XX PF 21-FEB-2002; 2002WO-JP01563.
 XX PR 26-FEB-2001; 2001JP-0050297.
 XX PA (KOWA) KOWA CO LTD.
 XX PA (KAGA) CHEMO-SERO-THERAPEUTIC RES INST.
 XX PI Naruse H, Sano M, Shinoda Y, Inagi T;
 XX WPI; 2002-674988/72.
 XX DR Eye drops for treating e.g. corneal diseases, contain CPB-1 and
 XX PT polyhydric alcohol with specific carbonyl value, without unpleasant
 XX PT irritation upon dropping but with satisfactory long-term storability
 XX PS Disclosure; Page 13-14; 16pp; Japanese.
 CC The invention relates to eye drops contain CPB-1 (anexin V) and a
 CC polyhydric alcohol having a carbonyl value of not more than
 CC 5micro Mol /g. The eyes drops are for treating e.g. corneal diseases.

CC Such eye drops are without unpleasant irritation upon dropping but with
 CC satisfactory long-term storage stability. The present sequence is
 CC the human CPB-1 (calcium/phospholipid binding) protein.
 XX
 SQ Sequence 319 AA;

Query Match 43.4%; Score 1451.5; DB 23; Length 319;
 Best Local Similarity 91.5%; Pred. No. 2e-100;
 Matches 290; Conservative 12; Mismatches 14; Indels 1; Gaps 1;

QY 17 LRGTVDPSGFGDADAEVLKAMKGLGDEDSILNLTIRSNAGROQIAEERKTLFGRD 76
 DB 4 LRGTVDPSGFGDADAEVLKAMKGLGDEDSILNLTIRSNAGROQIAEERKTLFGRD 63
 QY 77 LVNDKSELTGKFEKTLVAMKPSRLYDAVELKAKLGAQDEKVTETIISRPEELRA 136
 DB 64 LDDDKSELTGKFEKTLVAMKPSRLYDAVELKAKLGAQDEKVTETIISRPEELRA 123
 QY 137 IKQAYEEYGSNLEDDVVGDTSGYQRMVLVLLQANRDPDAIDDAQVELDAQALFQAGE 196
 DB 124 IKQAYEEYGSNLEDDVVGDTSGYQRMVLVLLQANRDPDAIDDAQVELDAQALFQAGE 183
 QY 197 LKMGTEBEKFTITIGTSVSHLRVPDKYMTISGFOIETIDRETSGNLEQLLAVKSI 256
 DB 184 LKMGTEBEKFTITIGTSVSHLRVPDKYMTISGFOIETIDRETSGNLEQLLAVKSI 243
 QY 257 RSIPAYLAETLYYAMKAGTDHDTLIRVIVSRSEIDLEFNIRKFRKPFATSLYSMTKGD 316
 DB 244 RSIPAYLAETLYYAMKAGTDHDTLIRVIVSRSEIDLEFNIRKFRKPFATSLYSMTKGD 303
 QY 317 SGDYKRALLLCGGDD 333
 DB 304 SGDYKRALLLCGGDD 319

RESULT 15
 AAP80511
 ID AAP80511 standard; protein; 320 AA.

XX AC AAP80511;
 XX DT 25-MAR-2003 (updated)
 XX DT 10-MAR-2003 (updated)
 XX DT 12-NOV-1990 (first entry)
 XX DE Placental coagulation inhibitor.
 XX KW Placental coagulation inhibitor; disseminated vascular coagulation;
 XX KW thrombosis.
 XX OS Homo sapiens.
 XX EN EP279459-A.
 XX EN JP03219875-A.
 XX PD 24-AUG-1988.
 XX PF 19-FEB-1988; 88EP-0102468.
 XX PR 20-FEB-1987; 87JP-0037227.
 XX PR 23-JUL-1987; 87JP-0184428.
 XX PA (KOWA) KOWA CO LTD.
 XX PI Sano Y, Iwasaki A, Suda M;
 XX WPI; 1988-236733/34.
 XX WPI; 1991-329110/45.
 XX N-PSDB; AAN81113.
 XX Recombinant placental coagulation inhibitor - useful for the prevention
 XX and treatment of thromboses or disseminated intra-vascular coagulation.

PS Disclosure; Page 2; 7pp; English.

XX
CC This polypeptide exhibits strong anticoagulant activities and is useful
CC for the treatment and prevention of e.g. thrombosis or disseminated
CC intravascular coagulation in the brain, heart and peripheral blood
CC vessels, such as cerebral and myocardial infarction. It has no
CC antigenicity against man and can be produced in large amounts using
CC recombinant methods.
CC (Updated on 10-MAR-2003 to add missing OS field.)
CC (Updated on 25-MAR-2003 to correct PF field.)
CC (Updated on 25-MAR-2003 to correct PR field.)
CC (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ Sequence 320 AA;

Query Match 43.4%; Score 1451.5; DB 9; Length 320;

Best Local Similarity 91.5%; Pred. No. 2e-100;
Matches 290; Conservative 12; Mismatches 14; Indels 1; Gaps 1;

QY	17	LRGTVDPSGFDGRADAETLRKAMKGLGTDDESIINLLTARSNAQROQIAEEFKTLFGPD	76
Db	5	LRGTVDPSGFDGRADAETLRKAMKGLGTDDESIINLLTARSNAQROQISAFKTLFGPD	64
QY	77	LVDNKSSELTGKPEKLIVALMKPSRLYDAVEELKAKLGAQDEKVLTEIISRTPEELRA	136
Db	65	LDDLSSELTGKPEKLIVALMKPSRLYDAVEELKAKLGAQDEKVLTEIISRTPEELRA	124
QY	137	IKOAYEEKSNLEDDVVDTSYGYORMVLLQANRDPDAIDDAQVELDAQALFOAGE	196
Db	125	IKOYDEEYSSLEDDVVDTSYGYORMVLLQANRDPDAIDDAQVELDAQALFOAGE	184
QY	197	LKMGTDDEKIIITIGTRSVSHLRVVDKMYTISGFQIETIDRETSGNLEMLLAVVSI	256
Db	185	LKMGTDDEKIIITIGTRSVSHLRVVDKMYTISGFQIETIDRETSGNLEMLLAVVSI	244
QY	257	RSTPAYLAETLYAMKAGTDDHTLIRVVSSEIDLPIRKEFRKNPATSLYSNIKGD	316
Db	245	RSTPAYLAETLYAMKAGTDDHTLIRVVSSEIDLPIRKEFRKNPATSLYSNIKGD	304
QY	317	SGDYKXALLLLCGEDD	333
Db	305	SGDYKXALLLLC-GEED	320

Search completed: December 12, 2003, 14:50:03
Job time : 53.1387 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OK protein - protein search, using sw model

Run on: December 12, 2003, 14:50:08 ; Search time 37.2419 Seconds

(without alignments)
3340.943 Million cell updates/sec

Title: PCT-US03-24332-6

Perfect score: 3343

Sequence: 1 MDYKDDDDKLAANXALRGT.....GDTSGDYKKALLLCGSHD 669

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 684280 seqs, 185983659 residues

Total number of hits satisfying chosen parameters: 684280

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3337	99.8	669	12 US-10-080-370-6	Sequence 6, Appl1
2	1593	47.7	319	12 US-10-080-370-3	Sequence 3, Appl1
3	1451.5	43.4	320	14 US-10-007-761-72	Sequence 72, Appl1
4	1442.5	43.1	327	10 US-09-970-969-2	Sequence 2, Appl1
5	1442.5	43.1	327	10 US-09-970-969-4	Sequence 4, Appl1
6	1442.5	43.1	327	10 US-09-970-969-6	Sequence 6, Appl1
7	921	27.6	321	15 US-10-097-340-10	Sequence 10, Appl1
8	827	27.6	324	9 US-09-925-301-1062	Sequence 1062, Appl1
9	827	26.5	208	9 US-09-925-302-731	Sequence 731, Appl1
10	822.5	24.6	327	12 US-10-236-031B-18	Sequence 18, Appl1
11	790	23.5	324	12 US-10-316-253-262	Sequence 262, Appl1
12	785	23.5	323	15 US-10-205-823-34	Sequence 34, Appl1
13	763.5	22.8	485	10 US-09-925-300-1664	Sequence 1664, Appl1
14	695.5	20.8	339	10 US-09-974-298-91	Sequence 91, Appl1
15	695.5	20.8	339	15 US-10-097-340-6	Sequence 6, Appl1

16	695.5	20.8	339	15 US-10-097-340-8	Sequence 8, Appl1
17	678	20.3	327	9 US-09-764-853-615	Sequence 615, Appl1
18	675	20.2	332	11 US-09-764-881-110	Sequence 110, Appl1
19	647.5	19.4	319	15 US-10-304-287-2	Sequence 2, Appl1
20	632	18.9	373	9 US-09-925-301-888	Sequence 888, Appl1
21	628	18.8	346	10 US-09-919-172-39	Sequence 39, Appl1
22	628	18.7	346	10 US-09-974-298-93	Sequence 93, Appl1
23	625	18.7	346	10 US-10-316-253-300	Sequence 300, Appl1
24	381.5	11.4	289	9 US-09-925-301-597	Sequence 597, Appl1
25	376.5	11.3	316	15 US-10-219-220-260	Sequence 260, Appl1
26	374.5	11.2	316	15 US-10-219-220-62	Sequence 62, Appl1
27	316	9.5	158	9 US-09-925-297-479	Sequence 479, Appl1
28	237.5	7.1	239	15 US-10-219-220-65	Sequence 65, Appl1
29	223.5	6.7	319	12 US-10-259-165-56	Sequence 56, Appl1
30	223.5	6.7	319	12 US-10-259-165-402	Sequence 402, Appl1
31	222	6.6	336	12 US-10-259-165-290	Sequence 290, Appl1
32	221	6.6	184	15 US-10-219-220-66	Sequence 66, Appl1
33	147.5	4.4	701	9 US-09-815-242-13002	Sequence 13002, A
34	141	4.2	82	9 US-09-925-301-1467	Sequence 1467, Ap
35	131	3.9	617	9 US-09-815-242-5762	Sequence 5762, Ap
36	130.5	3.9	1786	10 US-09-712-096-3	Sequence 3, Appl1
37	129	3.9	872	14 US-10-047-260-38	Sequence 38, Appl1
38	127.5	3.8	1004	10 US-09-738-626-5676	Sequence 5676, Ap
39	127.5	3.8	1007	11 US-09-957-005-9	Sequence 9, Appl1
40	127	3.8	2099	15 US-10-128-714-3290	Sequence 3290, Ap
41	127	3.8	2405	15 US-10-128-714-8290	Sequence 8290, Ap
42	125.5	3.8	457	9 US-09-815-242-12670	Sequence 12670, A
43	123	3.7	810	12 US-09-769-744A-74	Sequence 74, Appl1
44	122.5	3.7	862	15 US-10-177-293-391	Sequence 391, Appl1
45	122	3.6	46	12 US-10-029-386-30160	Sequence 30160, A

ALIGNMENTS

RESULT 1
US-10-080-370-6
; Sequence 6, Application US/10080370
; Publication No. US20030166532A1
; GENERAL INFORMATION:
; APPLICANT: Allison, Anthony
; TITLE OF INVENTION: Modified Annexin Proteins and Methods for Preventing Thrombosis
; FILE REFERENCE: SUPP.30
; CURRENT APPLICATION NUMBER: US/10/080,370
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/270,402
; PRIOR FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: 60/332,582
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 669
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURES:
; NAME/KEY: misc_feature
; LOCATION: (15)..(15)
; OTHER INFORMATION: The 'Xaa' at location 15 stands for Ser.
; NAME/KEY: misc_feature
; LOCATION: (334)..(334)
; OTHER INFORMATION: The 'Xaa' at location 334 stands for Lys, Arg, Ser, Thr.
; OTHER INFORMATION: Tyr, Trp, Cys, or Phe.
; NAME/KEY: misc_feature
; LOCATION: (351)..(351)
; OTHER INFORMATION: The 'Xaa' at location 351 stands for Lys, Asn, Arg, Ser, Thr.
; OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop cod
; OTHER INFORMATION: Tyr, Trp, Cys, or Phe.
; NAME/KEY: misc_feature
; LOCATION: (45)..(45)
; OTHER INFORMATION: n = a, c, g, or t

NAME/KEY: misc.feature
 LOCATION: (1000)..(1002)
 OTHER INFORMATION: n = a, c, g, or t
 NAME/KEY: misc.feature
 LOCATION: (1051)..(1053)
 OTHER INFORMATION: n = a, c, g, or t
 US-10-080-370-6

Query Match 99.8%; Score 3337; DB 12; Length 669;
 Best Local Similarity 100.0%; Pred. No. 2,9e-268;
 Matches 669; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYKDDDKLAANYALRGVITDTSFGDGRDAEVLTKKAKGLGTDEDSILNLTARSA 60
 DB 1 MDYKDDDKLAANYALRGVITDTSFGDGRDAEVLTKKAKGLGTDEDSILNLTARSA 60
 QY 61 OROQIAEEFKTLFGSDLVNDKSELTKGFEKLIYALMKPSRLYDAVELKAKLGAAGTDEK 120
 DB 61 OROQIAEEFKTLFGSDLVNDKSELTKGFEKLIYALMKPSRLYDAVELKAKLGAAGTDEK 120
 QY 121 VLTEIIASRTPEELRAIKOAYEEYGSNLEDDVVGDTSGYQRMVLLQANRDPPTAID 180
 DB 121 VLTEIIASRTPEELRAIKOAYEEYGSNLEDDVVGDTSGYQRMVLLQANRDPPTAID 180
 QY 181 DAQVELDAQALFOAGELKMGTEDEKFTTILGTSVSHLRVFPKMTTISGFOEETIDRE 240
 DB 181 DAQVELDAQALFOAGELKMGTEDEKFTTILGTSVSHLRVFPKMTTISGFOEETIDRE 240
 QY 241 TSGNLEMLLAVKSIISIPAYLAETLYAMKAGTDDHTLIRIVSRSEIDLFINRKEF 300
 DB 241 TSGNLEMLLAVKSIISIPAYLAETLYAMKAGTDDHTLIRIVSRSEIDLFINRKEF 300
 QY 301 RKNPATSISYMKIGDTSQDYKALLLCCGSEDYKRSRSGLEVLFGPGSTXALRGVTDF 360
 DB 301 RKNPATSISYMKIGDTSQDYKALLLCCGSEDYKRSRSGLEVLFGPGSTXALRGVTDF 360
 QY 361 SGFGRADAELVLRKAMKGLGTDEDSILNLTARSNARQOIAEEFKTLFGSDLVNDKSE 420
 DB 361 SGFGRADAELVLRKAMKGLGTDEDSILNLTARSNARQOIAEEFKTLFGSDLVNDKSE 420
 QY 421 LTGFEKLIYALMKPSRLYDAVELKAKLGAAGTDEKLTETIIASRTPEELRAIKOAYEE 480
 DB 421 LTGFEKLIYALMKPSRLYDAVELKAKLGAAGTDEKLTETIIASRTPEELRAIKOAYEE 480
 QY 481 YGSNLEDDVVGDTSGYQRMVLLQANRDPPTAIDDAQVELDAQALFOAGELKMGTEDE 540
 DB 481 YGSNLEDDVVGDTSGYQRMVLLQANRDPPTAIDDAQVELDAQALFOAGELKMGTEDE 540
 QY 541 KFTTILGTSVSHLRVFPKMTTISGFOEETIDRETSNLEMLLAVKSIISIPAYLA 600
 DB 541 KFTTILGTSVSHLRVFPKMTTISGFOEETIDRETSNLEMLLAVKSIISIPAYLA 600
 QY 601 ETLVYAMKAGTDDHTLIRIVSRSEIDLFINRKEKRNKPFATLSYMKIGDTSQDYKAL 660
 DB 601 ETLVYAMKAGTDDHTLIRIVSRSEIDLFINRKEKRNKPFATLSYMKIGDTSQDYKAL 660
 QY 661 LLLCGGEDD 669
 DB 661 LLLCGGEDD 669

RESULT 2
 US-10-080-370-3

; Sequence 3, Application US/10080370
 ; Publication No. US20030166532A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Allison, Anthony
 ; TITLE OF INVENTION: Modified Annexin Proteins and Methods for Preventing Thrombosis
 ; FILE REFERENCE: SORR 90
 ; CURRENT APPLICATION NUMBER: US/10/080,370
 ; CURRENT FILING DATE: 2002-02-21
 ; PRIOR APPLICATION NUMBER: 60/270,402
 ; PRIOR FILING DATE: 2001-02-21

PRIOR APPLICATION NUMBER: 60/332,582
 ; PRIOR FILING DATE: 2001-11-21
 ; NUMBER OF SEQ ID NOS: 9
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 3
 ; LENGTH: 319
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-080-370-3

Query Match 47.7%; Score 1593; DB 12; Length 319;
 Best Local Similarity 100.0%; Pred. No. 4.4e-124;
 Matches 319; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 ALRGVTDFSGFGRDAEVLTKKAKGLGTDEDSILNLTARSNARQOIAEEFKTLFG 75
 DB 2 ALRGVTDFSGFGRDAEVLTKKAKGLGTDEDSILNLTARSNARQOIAEEFKTLFG 75
 QY 76 DLVNDKSELTKGFEKLIYALMKPSRLYDAVELKAKLGAAGTDEKLTETIIASRTPEEL 135
 DB 76 DLVNDKSELTKGFEKLIYALMKPSRLYDAVELKAKLGAAGTDEKLTETIIASRTPEEL 135
 QY 136 AIKOAYEEYGSNLEDDVVGDTSGYQRMVLLQANRDPPTAIDDAQVELDAQALFOAG 195
 DB 136 AIKOAYEEYGSNLEDDVVGDTSGYQRMVLLQANRDPPTAIDDAQVELDAQALFOAG 195
 QY 196 ELKMGTEDEKFTTILGTSVSHLRVFPKMTTISGFOEETIDRETSNLEMLLAVKS 255
 DB 196 ELKMGTEDEKFTTILGTSVSHLRVFPKMTTISGFOEETIDRETSNLEMLLAVKS 255
 QY 256 IRSIPAYLAETLYAMKAGTDDHTLIRIVSRSEIDLFINRKEKRNKPFATLSYMKIGD 315
 DB 256 IRSIPAYLAETLYAMKAGTDDHTLIRIVSRSEIDLFINRKEKRNKPFATLSYMKIGD 315
 QY 316 TSGDYKALLLCCGSED 333
 DB 302 TSGDYKALLLCCGSED 315

RESULT 3

US-10-007-761-72
 ; Sequence 72, Application US/10007761
 ; Publication No. US20020150984A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Mochly-Rosen, David
 ; TITLE OF INVENTION: Peptides for Activation and Inhibition
 ; FILE REFERENCE: of delta-PKC
 ; CURRENT APPLICATION NUMBER: US/10/007,761
 ; CURRENT FILING DATE: 2001-11-09
 ; PRIOR APPLICATION NUMBER: US 60/262,060
 ; PRIOR FILING DATE: 2001-01-18
 ; NUMBER OF SEQ ID NOS: 72
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 72
 ; LENGTH: 320
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-007-761-72

Query Match 43.4%; Score 1451.5; DB 14; Length 320;
 Best Local Similarity 91.5%; Pred. No. 2.4e-112;
 Matches 290; Conservative 12; Mismatches 14; Indels 1; Gaps 1;

QY 17 LRGTVDPSGFGGRDAEVLTKKAKGLGTDEDSILNLTARSNARQOIAEEFKTLFG 76
 DB 5 LRGTVDPSGFGGRDAEVLTKKAKGLGTDEDSILNLTARSNARQOIAEEFKTLFG 76
 QY 77 LVNDKSELTKGFEKLIYALMKPSRLYDAVELKAKLGAAGTDEKLTETIIASRTPEEL 136
 DB 65 LVNDKSELTKGFEKLIYALMKPSRLYDAVELKAKLGAAGTDEKLTETIIASRTPEEL 136
 QY 137 IKOAYEEYGSNLEDDVVGDTSGYQRMVLLQANRDPPTAIDDAQVELDAQALFOAG 196

Db 125 IKQVEEYEGSSLEDDVVGDTSGYQRMVLVLLQANRPDPDAGIDEAQVEBDAQALFQAGE 184
QY 197 LKMGDEEKFITITLGRSVSHLRVFDKXMTISGFQIEETIDRETSGNLEMLLAAYKSI 256
Db 185 LKMGDEEKFITIFGRSVSHLRKVFDDKXMTISGFQIEETIDRETSGNLEMLLAAYKSI 244
QY 257 RSIIPAYLAETLYAAKAGAGTDHDLIRIVSRSEIDLFINRKEFRKPFATSLYSWIKGDT 316
Db 245 RSIIPAYLAETLYAAKAGAGTDHDLIRVWVSRSEIDLFINRKEFRKPFATSLYSWIKGDT 304
QY 317 SGDYYKALLLGCSEDD 333
Db 305 SGDYYKALLLGCSEDD 320

RESULT 4
US-09-970-969-2

/ Sequence 2, Application US/09970969
/ Patent No. US20020103341A1
/ GENERAL INFORMATION:
/ APPLICANT: Tait, Jonathan F.
/ TITLE OF INVENTION: Annexin Derivatives with Endogenous Chelation Sites
/ FILE REFERENCE: u01w-1-13841
/ CURRENT APPLICATION NUMBER: US/09/970,969
/ CURRENT FILING DATE: 2001-10-03
/ NUMBER OF SEQ ID NOS: 6
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 2
/ LENGTH: 327
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-970-969-2

Query Match 43.1%; Score 1442.5; DB 10; Length 327;
Best Local Similarity 91.2%; Pred. No. 1.4e-111;
Matches 289; Conservative 12; Mismatches 15; Indels 1; Gaps 1;

QY 17 LRGTVTFSGFDGADAEVLRKAMKGLGTDSDSILNLTARSNAQOQIAEFKTLFGSD 76
Db 12 LRGTVTFSGFDGADAEVLRKAMKGLGTDSDSILNLTARSNAQOQIAEFKTLFGSD 71
QY 77 LNDKMSLTGKFEKLIYALMKPSRLYDAYELKHAUKAGAGTDEKVLTEIIASRTPEELRA 136
Db 72 LNDKMSLTGKFEKLIYALMKPSRLYDAYELKHAUKAGAGTDEKVLTEIIASRTPEELRA 131
QY 137 IKQAVEEYEGSSNLEDDVVGDTSGYQRMVLVLLQANRPDPDAGIDEAQVEBDAQALFQAGE 196
Db 132 IKQAVEEYEGSSNLEDDVVGDTSGYQRMVLVLLQANRPDPDAGIDEAQVEBDAQALFQAGE 191
QY 197 LKMGDEEKFITITLGRSVSHLRVFDKXMTISGFQIEETIDRETSGNLEMLLAAYKSI 256
Db 192 LKMGDEEKFITIFGRSVSHLRKVFDDKXMTISGFQIEETIDRETSGNLEMLLAAYKSI 251
QY 257 RSIIPAYLAETLYAAKAGAGTDHDLIRIVSRSEIDLFINRKEFRKPFATSLYSWIKGDT 316
Db 252 RSIIPAYLAETLYAAKAGAGTDHDLIRVWVSRSEIDLFINRKEFRKPFATSLYSWIKGDT 311
QY 317 SGDYYKALLLGCSEDD 333
Db 312 SGDYYKALLLGCSEDD 327

RESULT 5
US-09-970-969-4
/ Sequence 4, Application US/09970969
/ Patent No. US20020103341A1
/ GENERAL INFORMATION:
/ APPLICANT: Tait, Jonathan F.
/ APPLICANT: Brown, David S.
/ TITLE OF INVENTION: Annexin Derivatives with Endogenous Chelation Sites
/ FILE REFERENCE: u01w-1-13841

/ CURRENT APPLICATION NUMBER: US/09/970,969
/ CURRENT FILING DATE: 2001-10-03
/ NUMBER OF SEQ ID NOS: 6
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 4
/ LENGTH: 327
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-970-969-4

Query Match 43.1%; Score 1442.5; DB 10; Length 327;
Best Local Similarity 91.2%; Pred. No. 1.4e-111;
Matches 289; Conservative 12; Mismatches 15; Indels 1; Gaps 1;

QY 17 LRGTVTFSGFDGADAEVLRKAMKGLGTDSDSILNLTARSNAQOQIAEFKTLFGSD 76
Db 12 LRGTVTFSGFDGADAEVLRKAMKGLGTDSDSILNLTARSNAQOQIAEFKTLFGSD 71
QY 77 LNDKMSLTGKFEKLIYALMKPSRLYDAYELKHAUKAGAGTDEKVLTEIIASRTPEELRA 136
Db 72 LNDKMSLTGKFEKLIYALMKPSRLYDAYELKHAUKAGAGTDEKVLTEIIASRTPEELRA 131
QY 137 IKQAVEEYEGSSNLEDDVVGDTSGYQRMVLVLLQANRPDPDAGIDEAQVEBDAQALFQAGE 196
Db 132 IKQAVEEYEGSSNLEDDVVGDTSGYQRMVLVLLQANRPDPDAGIDEAQVEBDAQALFQAGE 191
QY 197 LKMGDEEKFITITLGRSVSHLRVFDKXMTISGFQIEETIDRETSGNLEMLLAAYKSI 256
Db 192 LKMGDEEKFITIFGRSVSHLRKVFDDKXMTISGFQIEETIDRETSGNLEMLLAAYKSI 251
QY 257 RSIIPAYLAETLYAAKAGAGTDHDLIRIVSRSEIDLFINRKEFRKPFATSLYSWIKGDT 316
Db 252 RSIIPAYLAETLYAAKAGAGTDHDLIRVWVSRSEIDLFINRKEFRKPFATSLYSWIKGDT 311
QY 317 SGDYYKALLLGCSEDD 333
Db 312 SGDYYKALLLGCSEDD 327

RESULT 6
US-09-970-969-6
/ Sequence 6, Application US/09970969
/ Patent No. US20020103341A1
/ GENERAL INFORMATION:
/ APPLICANT: Tait, Jonathan F.
/ APPLICANT: Brown, David S.
/ TITLE OF INVENTION: Annexin Derivatives with Endogenous Chelation Sites
/ FILE REFERENCE: u01w-1-13841
/ CURRENT APPLICATION NUMBER: US/09/970,969
/ CURRENT FILING DATE: 2001-10-03
/ NUMBER OF SEQ ID NOS: 6
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 6
/ LENGTH: 327
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-970-969-6

Query Match 43.1%; Score 1442.5; DB 10; Length 327;
Best Local Similarity 91.2%; Pred. No. 1.4e-111;
Matches 289; Conservative 12; Mismatches 15; Indels 1; Gaps 1;

QY 17 LRGTVTFSGFDGADAEVLRKAMKGLGTDSDSILNLTARSNAQOQIAEFKTLFGSD 76
Db 12 LRGTVTFSGFDGADAEVLRKAMKGLGTDSDSILNLTARSNAQOQIAEFKTLFGSD 71
QY 77 LNDKMSLTGKFEKLIYALMKPSRLYDAYELKHAUKAGAGTDEKVLTEIIASRTPEELRA 136
Db 72 LNDKMSLTGKFEKLIYALMKPSRLYDAYELKHAUKAGAGTDEKVLTEIIASRTPEELRA 131
QY 137 IKQAVEEYEGSSNLEDDVVGDTSGYQRMVLVLLQANRPDPDAGIDEAQVEBDAQALFQAGE 196
Db 132 IKQAVEEYEGSSNLEDDVVGDTSGYQRMVLVLLQANRPDPDAGIDEAQVEBDAQALFQAGE 191

```

QY 197 LKMGDEKFTITLIGTSVSHLRVFPKXMTISGFOJETIDRETSNGNLENTLLAVVKS1 256
DB 192 LKMGDEKFTITIGTSVSHLRVFPKXMTISGFOJETIDRETSNGNLENTLLAVVKS1 251
QY 257 RSPAYLAETLYAMKAGAGTDHTLIRVIVSRSEIDLFNIRKEFRKNFATSYSMTKQDT 316
DB 252 RSPAYLAETLYAMKAGAGTDHTLIRVIVSRSEIDLFNIRKEFRKNFATSYSMTKQDT 311
QY 317 SGDYKXALLLCGGEDD 333
DB 312 SGDYKXALLLCGGEDD 327

RESULT 7
US-10-097-340-10
; Sequence 10, Application US/10097340
; Publication No. US20030087250A1
; GENERAL INFORMATION:
; APPLICANT: John MOWHAN
; APPLICANT: Manjula GANNANVARAPU
; APPLICANT: Sebastian HOERSCH
; APPLICANT: Shubhangt KAMATKAR
; APPLICANT: Steve G KOVATS
; APPLICANT: Rachel E. MEYERS
; APPLICANT: Michael MORRISSEY
; APPLICANT: Peter OLANDT
; APPLICANT: Ami SEN
; APPLICANT: Peter VEIRY
; APPLICANT: Gordon B. MILLS
; APPLICANT: Robert C. BAST, Jr.
; APPLICANT: Karen LU
; APPLICANT: Rosemarie SCHMANDT
; APPLICANT: Xumei ZHAO
; TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,
; TITLE OF INVENTION: Assessment, Prevention, and Therapy of Ovarian Cancer
; FILE REFERENCE: MRI-030
; CURRENT APPLICATION NUMBER: US/10/097,340
; PRIOR FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: 60/276,025
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/325,149
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/276,026
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/324,967
; PRIOR FILING DATE: 2001/09/26
; PRIOR APPLICATION NUMBER: 60/311,732
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/325,102
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/323,580
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 321
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-097-340-10

Query Match 27.6%; Score 921; DB 15; Length 321;
Best Local Similarity 57.3%; Pred. No. 2,4e-68;
Matches 180; Conservative 56; Mismatches 78; Indels 0; Gaps 0;
QY 19 GTVDFSGFGRDAEVLIRKAMKGLGTDEDSINLITANSNAQOQIAEEFTLFGRLDV 78
DB 8 GTVKAASGFNAMEDAQTLIRKAMKGLGTDEDAIISVLAIRNTAQROEIRTAYSKTIGRDLI 67
QY 79 NDKKSELTGKFEKLIYALMKPSRLYDAVELKHAUKGAGTDEKVTLEIIASRTPEELRAIK 138
DB 68 DTKSELISGNFEQYIVGMPTVLYDVQELRRAMKAGAGTDEGLIILASRTPEELRRIS 127

```

```

QY 139 QAYEEYGSNLEDDVVGDTSGYVQRMVYLLOANDPPTAIDDAQVEIDAAQLFOAGELK 198
DB 128 QTYOQOIGSLEDDISDTSFWMFORVLSLAGSDSENNYDDALVRDADDLVEAGBKK 187
QY 199 WGTDEKFTITLIGTSVSHLRVFPKXMTISGFOJETIDRETSNGNLENTLLAVVKSIRS 258
DB 188 WGTDEKFTLVLCSRRNHLHVPEYKRIKSGKDIEGSIKSETSGSFEDALALVKKCRN 247
QY 259 IPAYLAETLYAMKAGAGTDHTLIRVIVSRSEIDLFNIRKEFRKNFATSYSMTKQDTSG 318
DB 248 KSAVFAEKLYKSKMKGITDNTLIRVIVSRSEIDLFNIRKEFRKNFATSYSMTKQDTSG 307
QY 319 DYKXALLLCGGED 332
DB 308 DYKXALLLCGGED 321

RESULT 8
US-09-925-301-1062
; Sequence 1062, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA106
; CURRENT APPLICATION NUMBER: US/09/925,301
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05882
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1062
; LENGTH: 324
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-301-1062

Query Match 27.6%; Score 921; DB 9; Length 324;
Best Local Similarity 57.3%; Pred. No. 2,5e-68;
Matches 180; Conservative 56; Mismatches 78; Indels 0; Gaps 0;
QY 19 GTVDFSGFGRDAEVLIRKAMKGLGTDEDSINLITANSNAQOQIAEEFTLFGRLDV 78
DB 11 GTVKAASGFNAMEDAQTLIRKAMKGLGTDEDAIISVLAIRNTAQROEIRTAYSKTIGRDLI 70
QY 79 NDKKSELTGKFEKLIYALMKPSRLYDAVELKHAUKGAGTDEKVTLEIIASRTPEELRAIK 138
DB 71 DTKSELISGNFEQYIVGMPTVLYDVQELRRAMKAGAGTDEGLIILASRTPEELRRIS 130
QY 139 QAYEEYGSNLEDDVVGDTSGYVQRMVYLLOANDPPTAIDDAQVEIDAAQLFOAGELK 198
DB 131 QTYOQOIGSLEDDISDTSFWMFORVLSLAGSDSENNYDDALVRDADDLVEAGBKK 190
QY 199 WGTDEKFTITLIGTSVSHLRVFPKXMTISGFOJETIDRETSNGNLENTLLAVVKSIRS 258
DB 191 WGTDEKFTLVLCSRRNHLHVPEYKRIKSGKDIEGSIKSETSGSFEDALALVKKCRN 250
QY 259 IPAYLAETLYAMKAGAGTDHTLIRVIVSRSEIDLFNIRKEFRKNFATSYSMTKQDTSG 318
DB 251 KSAVFAEKLYKSKMKGITDNTLIRVIVSRSEIDLFNIRKEFRKNFATSYSMTKQDTSG 310
QY 319 DYKXALLLCGGED 332
DB 311 DYKXALLLCGGED 324

```

GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA104
CURRENT APPLICATION NUMBER: US/09/925,302
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05918
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 896
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 731
LENGTH: 208
TYPE: PRT
ORGANISM: Homo sapiens
US-09-925-302-731

Query Match 26.5%; Score 887; DB 9; Length 208;
Best Local Similarity 85.9%; Pred. No. 8,6e-66;
Matches 177; Conservative 11; Mismatches 18; Indels 0; Gaps 0;

QY 10 LAAANXALRGTVDFSGDGRADAELVRKAMKGLGTDEDSILNLTARSMARQOIAREF 69
DB 1 VVAQAQVLRGTIVDFSGDGRADAELVRKAMKGLGTDEDSILNLTARSMARQOISAF 60
QY 70 KTLFGRDLVNDKSELTGKFEKLIYALMKPSRLYDAVELKHAUKGAGTDEKVLTEIIASR 129
DB 61 KTLFGRDLVNDKSELTGKFEKLIYALMKPSRLYDAVELKHAUKGAGTDEKVLTEIIASR 120
QY 130 TPEELRAIKQAYEEBEGSNLEDDVVDTSQYQRMVLLQANRPDPAIDDAQVELDAQ 189
DB 121 TPEELRAIKQAYEEBEGSNLEDDVVDTSQYQRMVLLQANRPDPAIDDAQVELDAQ 180
QY 190 ALFOAGELKMGTDSEKFTILGTRSV 215
DB 181 ALFOAGELKMGTDSEKFTILGTRSV 206

RESULT 10
US-10-236-031B-18
Sequence 18; Application US/10236031B
Publication No. US20030219760A1
GENERAL INFORMATION:
APPLICANT: Gordon, Gavin J.
APPLICANT: Jensen, Roderick V.
APPLICANT: Gullans, Steven R.
APPLICANT: Bueno, Raphael
TITLE OF INVENTION: Diagnostic and Prognostic Tests
FILE REFERENCE: B00801/70265 (JRV/JAV)
CURRENT APPLICATION NUMBER: US/10/236, 031B
CURRENT FILING DATE: 2002-09-05
PRIOR APPLICATION NUMBER: US 60/317,389
PRIOR FILING DATE: 2001-09-05
PRIOR APPLICATION NUMBER: US 60/407,431
PRIOR FILING DATE: 2002-08-30
NUMBER OF SEQ ID NOS: 102
SOFTWARE: PatentIn version 3.1
SEQ ID NO 18
LENGTH: 327
TYPE: PRT
ORGANISM: Homo sapiens
US-10-236-031B-18

Query Match 24.6%; Score 822.5; DB 12; Length 327;
Best Local Similarity 56.9%; Pred. No. 3.7e-60;
Matches 178; Conservative 44; Mismatches 90; Indels 1; Gaps 1;

QY 20 TVNDFSGDGRADAELVRKAMKGLGTDEDSILNLTARSMARQOIAREF 79
DB 14 TVSSSHFNDPDAELVLRKAMKGLGTDEDSILNLTARSMARQOIAREF 73
QY 80 DKSELTGKFEKLIYALMKPSRLYDAVELKHAUKGAGTDEKVLTEIIASRTPEELRAIKQ 139

DB 74 TLKSELGFEELIYALMTPPVYAKLHDMKGLGTKEGVITIELISRTNOLREIMK 133
QY 140 AYEBSYGNLEDDVVDTSQYQRMVLLQANRPDPAIDDAQVELDAQFOAGELK 198
DB 134 AYEBSYGNLEDDVVDTSQYQRMVLLQANRPDPAIDDAQVELDAQFOAGELK 193
QY 199 WGTDEKFTITIGTSVSHLRVPKMTTIGSFQLEETIDETSGNLENNLAVYSIRS 256
DB 194 RGTDEKFTITIGTSVSHLRVPKMTTIGSFQLEETIDETSGNLENNLAVYSIRS 253
QY 259 IPAYLAETIYAMKAGTDDHTLIRVYSRSEIDLFRKFRKXNATSLYSMTKGTSG 316
DB 254 LHSYFAERLYAMKAGTDDHTLIRVYSRSEIDLFRKFRKXNATSLYSMTKGTSG 313
QY 319 DYKALLILCGGE 331
DB 314 DYKALLILCGGE 326

RESULT 11
US-10-316-253-262
Sequence 262; Application US/10316253
Publication No. US20030162706A1
GENERAL INFORMATION:
APPLICANT: The Procter & Gamble Company
APPLICANT: Peters, Kevin
APPLICANT: Thompson, Larry
APPLICANT: Wang, Feng
APPLICANT: Greis, Kenneth
TITLE OF INVENTION: Angiogenesis Modulating Proteins
FILE REFERENCE: 8865M
CURRENT APPLICATION NUMBER: US/10/316,253
CURRENT FILING DATE: 2002-12-10
PRIOR APPLICATION NUMBER: US 60/355,295
PRIOR FILING DATE: 2002-02-08
NUMBER OF SEQ ID NOS: 308
SOFTWARE: PatentIn version 3.1
SEQ ID NO 262
LENGTH: 324
TYPE: PRT
ORGANISM: Rattus norvegicus
US-10-316-253-262

Query Match 23.6%; Score 790; DB 12; Length 324;
Best Local Similarity 47.9%; Pred. No. 1.8e-57;
Matches 156; Conservative 65; Mismatches 99; Indels 6; Gaps 1;

QY 343 LFGQPGSTYALRGTVDFSGDGRADAELVRKAMKGLGTDEDSILNLTARSMARQOIAREF 402
DB 5 LNWGP-----RGITNNYPGPNPSVDAEARKAIKGTDEKTLINILITERSNAQOILIV 58
QY 403 EEFKTLFGRDLVNDKSELTGKFEKLIYALMKPSRLYDAVELKHAUKGAGTDEKVLTEII 462
DB 59 KAIQAYEALKAADKGLSGHFEHWVALITAVADAKQKSMGAGTDEKVLTEII 118
QY 463 ASRTEELRAIKQAYEEBEGSNLEDDVVDTSQYQRMVLLQANRPDPAIDDAQVEL 522
DB 119 TTRTSRQMEKISQAYYAYKKNLDDISSFTSGDFRKALLTLADGGRDESLKVDHIAKK 178
QY 523 DAQALFOAGELKMGTDSEKFTILGTRSVSHLRVPKMTTIGSFQLEETIDETSGNLE 562
DB 179 DAQTYDAEKKMGTDSEKFTILGTRSVSHLRVPKMTTIGSFQLEETIDETSGNLE 228
QY 583 NULLAVYSIRSIPAYLAETIYAMKAGTDDHTLIRVYSRSEIDLFRKFRKXNATSLYSMTKGTSG 642
DB 239 DLLAVVACTRNTPAFLAGRLHQAUKGAGTDEFTLNIMVSRSEIDLIRPERKXNYGC 298
QY 643 SLYSMTKGTSGDYKALLILCGGE 668
DB 299 SLYSMTKGTSGDYKALLILCGGE 324


```

RESULT 12
US-10-205-823-34
; Sequence 34, Application US/10205823
; Publication No. US20030108963A1
GENERAL INFORMATION:
APPLICANT: Schlegel, Robert
APPLICANT: Monahan, John E.
APPLICANT: Endege, Wilson O.
APPLICANT: Gannavarapu, Manjula
APPLICANT: Gorbacheva, Bella
APPLICANT: Hoersch, Sebastian
APPLICANT: Kamatkar, Shubhangi
APPLICANT: Monsey, Angela M.
APPLICANT: Glatz, Karen
APPLICANT: Zhao, Xumei
APPLICANT: Anderson, Dustin
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAPY OF PROSTATE CANCER
FILE REFERENCE: MRI-044
CURRENT APPLICATION NUMBER: US/10/205,823
CURRENT FILING DATE: 2002-07-25
PRIOR APPLICATION NUMBER: 60/307,982
PRIOR FILING DATE: 2001-07-25
PRIOR APPLICATION NUMBER: 60/314,356
PRIOR FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/325,020
PRIOR FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: 60/341,746
PRIOR FILING DATE: 2001-12-12
PRIOR APPLICATION NUMBER: 60/362,158
PRIOR FILING DATE: 2002-03-05
NUMBER OF SEQ ID NOS: 455
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 34
LENGTH: 323
TYPE: PRT
ORGANISM: Homo sapiens
US-10-205-823-34

Query Match      23.5%; Score 785; DB 15; Length 323;
Best Local Similarity 48.3%; Pred. No. 4,6e-57;
Matches 152; Conservative 68; Mismatches 95; Indels 0; Gaps 0;

QY 18 RGTVDPSGDCGRADAEVLRKMKGLGTDEDSINLLTASNAQROIAEEFKTLPERDL 77
DB 9 RGTVDYPPFSPSPVDAEAIQKATRGIGTDEKXLSILTERSNAGQOLIVEYQAAVGGKEL 68
QY 78 VDMKSELTGKFEKLIYALMKPSRLYDAYEELKHAQLGAGTDEKVLTEIIASRTPEELRAI 137
DB 69 KDDLKGLDLSGFHEHLMVLPVPVFAKQKLSKMSKAGTVEADLITLITRISQVKDI 128
QY 138 KQAYEEYGSNLEDVVGDTSGYQRMVLVLQANRPDPTAIDQAVELDQALFOAGEL 197
DB 129 SQAVYTVYKKSIGDISSETSGDFRKALLTLADGRRESLKVDDHLAKQDAQILLYKAGEN 188
QY 198 KWTDEKEKIIITLGRSVSHLRVDPKMTISGFOIETTIDRTSGNLEMLLAVYSIR 257
DB 189 RMTGDEDKTEILCLRSFQKLTFDEVRNLSQDIYDSINGELSGHEDULLAIYACVR 248
QY 258 STPAYLAETLYAMGAGTDDHTLIRVYVSSEIDLENIRKEEFKATSLYSMTKGDTS 317
DB 249 NTPAFIAERLHRLALGIGDEFTLNIRIVSRSEIDLDIRTEFKHGYSLYSAIXSDTS 308
QY 318 GDYKALLLLCGGED 332
DB 309 GDYEITLTKICGGDD 323

```

```

GENERAL INFORMATION:
APPLICANT: Craig Rosen,
APPLICANT: Steve Ruben,
TITLE OF INVENTION: Nucleic Acids, Proteins and Anticodices
FILE REFERENCE: PA101
CURRENT APPLICATION NUMBER: US/09/925,300
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05988
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1890
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 1664
LENGTH: 485
TYPE: PRT
ORGANISM: Homo sapiens
US-09-925-300-1664

Query Match      22.8%; Score 763.5; DB 10; Length 485;
Best Local Similarity 45.6%; Pred. No. 5e-55;
Matches 154; Conservative 69; Mismatches 114; Indels 1; Gaps 1;

QY 329 GGEDDXSRSGLEVLFGGPGS-IXALRGITVTDPSGDCGRADAEVLRKMKGLGTDEDSL 387
DB 147 GGQWPSQYPGGQPTYPSPQPAVTQVGTGIRPANPDARDAEILRKMKGGTDEQATV 206
QY 388 NLTARSNAPROQIAEEFKTLFGRDLVNDKSELTKFEKLIYALMKPSRLYDAYEELKHA 447
DB 207 DVANRNSNDQROKIKAFKTSYQKDLJKLSLSNMBELLIALFMPPTYDANSLRA 266
QY 448 KLGGTDEKVLTEIIASRTPEELRAIKQAYEEYGSNLEDVVGDTSGYQRMVLVLLQA 507
DB 267 MGGAGTQERVLIELICTRWQEIETVRCYQSEFGHDLKDIRSDTSGHFEHLVSMCG 326
QY 508 NRDPDTAIDQAVELDQALFOAGELKMGDEKFTIITGTSVSHLRVDPKMTISGF 567
DB 327 NRDNQSNHMAQEDQRLYQEGRLGTDESCFMILATISFPOLRAITMAYSRMANR 386
QY 568 QIEETIDRTSGNLEMLLAVYSIRSPAYLAETLYAMGAGTDDHTLIRIVSRSEI 627
DB 387 DLTSSVEREFGYVESGLKTLIQCALNRPFAFERLYAMKAGTDDSTLVIRVTRSEI 446
QY 628 DLFNIRKEFRKNFRTSLYSMTKGDTSQYKALLLLCG 665
DB 447 DLVQIKQWFAQMTQKTLGTWAGTISGDYRRLHLAIVG 484

RESULT 14
US-09-974-298-91
; Sequence 91, Application US/09974298
; Patent No. US20020156263A1
GENERAL INFORMATION:
APPLICANT: Chen, Huel-Mei
TITLE OF INVENTION: GENES EXPRESSED IN BREAST CANCER
FILE REFERENCE: PA-0037 P
CURRENT APPLICATION NUMBER: US/09/974,298
CURRENT FILING DATE: 2001-10-04
PRIOR APPLICATION NUMBER: 60/238,331
PRIOR FILING DATE: 2000-05-10
NUMBER OF SEQ ID NOS: 194
SOFTWARE: PERL Program
SEQ ID NO 91
LENGTH: 339
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. US20020156263A1 1378745CD1
US-09-974-298-91

Query Match      20.8%; Score 695.5; DB 10; Length 339;
Best Local Similarity 45.4%; Pred. No. 1.3e-49;

```

Matches 143; Conservative 67; Mismatches 104; Indels 1; Gaps 1;

QY 19 GTYDFSGFDGRDAEVLKRAKMGGLTDEDSILNLTARSAQOQIAEEFKTLFGRLV 78
 Db 25 GSVKAYTNFPAERDANIETAIKTKGVDEVITVILNTRSAQRODIAFAVORRTKKELA 84
 QY 79 NDMKSELTKFEKFLIVALKMPSRLDYAYELGAHLGAGTDEKVLTEIIASRTPEELPAIK 136
 Db 85 SALKSALSGHLETVILGLKTPAQYDASELSKMGGLTDEDSLIEIICSTNOELQELIN 144
 QY 139 QAVEEYGSNLEDVVGDTSGYYQRLVLLQANRDPD-TAIDDAQVELDAQALFOAGEL 197
 Db 145 RYKEMKYTDLEKDIISDTSGDFRKLVMALAKGRRAEDGSVIDYELIDQDARDLYDAGVK 204
 QY 198 KMGTEBEKFTITLIGTSVSHLRVFDKMTISGFOIEETIDRETSGNLEMLLAVYSIR 257
 Db 205 RKGTDVPMKISIMTERSVPHLQKVFDRKYSYPYDMLSEIRKEVKGDLNFAFLNVQCIQ 264
 QY 258 SIPAYLAETLYYAMKAGTDDHTLIRIVSRSEIDLFINRKEFRKNFATSLYSIKGDTG 317
 Db 265 NKPLVFADRLYDSMKMGKGTDRDKVLIRIMVSRSEVDMKIRSEFRKXKGLYYITIQDITK 324
 QY 318 GDYKALLILCGGD 332
 Db 325 GDYKALLYLGGDD 339

RESULT 15

US-10-097-340-6

Sequence 6, Application US/10097340
 Publication No. US2003087250A1

GENERAL INFORMATION:

APPLICANT: John MONAHAN
 APPLICANT: Manjula GANNAVAPU
 APPLICANT: Sebastian HOERSCHE
 APPLICANT: Shubhangi KAMATKAR
 APPLICANT: Steve G. KOVATS
 APPLICANT: Rachel E. MEYERS
 APPLICANT: Michael MORRISSEY
 APPLICANT: Peter OLANDT
 APPLICANT: Aml SEN
 APPLICANT: Peter VERIBY
 APPLICANT: Gordon B. WILLS
 APPLICANT: Robert C. BAST, Jr.
 APPLICANT: Karen LY
 APPLICANT: Rosemarie SCHMANDT
 APPLICANT: Xumei ZHAO
 APPLICANT: Karen GLATT
 TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,
 FILE REFERENCE: MRI-030
 CURRENT APPLICATION NUMBER: US/10/097,340
 CURRENT FILING DATE: 2002-03-14
 PRIOR APPLICATION NUMBER: 60/276,025
 PRIOR FILING DATE: 2001-03-14
 PRIOR APPLICATION NUMBER: 60/325,149
 PRIOR FILING DATE: 2001-09-26
 PRIOR APPLICATION NUMBER: 60/276,026
 PRIOR FILING DATE: 2001-03-14
 PRIOR APPLICATION NUMBER: 60/324,967
 PRIOR FILING DATE: 2001/09/26
 PRIOR APPLICATION NUMBER: 60/311,732
 PRIOR FILING DATE: 2001-08-10
 PRIOR APPLICATION NUMBER: 60/325,102
 PRIOR FILING DATE: 2001-09-26
 PRIOR APPLICATION NUMBER: 60/323,580
 PRIOR FILING DATE: 2001-09-19
 NUMBER OF SEQ ID NOS: 363
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 6
 LENGTH: 339
 TYPE: PRT
 ORGANISM: Homo sapiens

US-10-097-340-6

Query Match 20.8%; Score 695.5; DB 15; Length 339;
 Best Local Similarity 45.4%; Pred. No. 1.3e-49;
 Matches 143; Conservative 67; Mismatches 104; Indels 1; Gaps 1;

QY 19 GTYDFSGFDGRDAEVLKRAKMGGLTDEDSILNLTARSAQOQIAEEFKTLFGRLV 78
 Db 25 GSVKAYTNFPAERDANIETAIKTKGVDEVITVILNTRSAQRODIAFAVORRTKKELA 84
 QY 79 NDMKSELTKFEKFLIVALKMPSRLDYAYELGAHLGAGTDEKVLTEIIASRTPEELPAIK 136
 Db 85 SALKSALSGHLETVILGLKTPAQYDASELSKMGGLTDEDSLIEIICSTNOELQELIN 144
 QY 139 QAVEEYGSNLEDVVGDTSGYYQRLVLLQANRDPD-TAIDDAQVELDAQALFOAGEL 197
 Db 145 RYKEMKYTDLEKDIISDTSGDFRKLVMALAKGRRAEDGSVIDYELIDQDARDLYDAGVK 204
 QY 198 KMGTEBEKFTITLIGTSVSHLRVFDKMTISGFOIEETIDRETSGNLEMLLAVYSIR 257
 Db 205 RKGTDVPMKISIMTERSVPHLQKVFDRKYSYPYDMLSEIRKEVKGDLNFAFLNVQCIQ 264
 QY 258 SIPAYLAETLYYAMKAGTDDHTLIRIVSRSEIDLFINRKEFRKNFATSLYSIKGDTG 317
 Db 265 NKPLVFADRLYDSMKMGKGTDRDKVLIRIMVSRSEVDMKIRSEFRKXKGLYYITIQDITK 324
 QY 318 GDYKALLILCGGD 332
 Db 325 GDYKALLYLGGDD 339

Search completed: December 12, 2003, 14:54:31
 Job time : 37.2419 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 12, 2003, 14:43:27 ; Search time 24.613 Seconds

(without alignments)
2036.647 Million cell updates/sec

Title: PCT-US03-24332-3

Perfect score: 1598

Sequence: 1 MALRGVTVPFGSGFGRADAE.....GDTSGDYKALLLCGGEHD 319

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Listing first 45 summaries

1: A_Geneseq_19Jun03.*
2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
3: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
4: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
5: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
6: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
7: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
8: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
9: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
10: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
11: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
12: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
13: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
14: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
15: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
16: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
17: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
18: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.*
19: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
20: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
21: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
25: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1598	100.0	319	24	ABP56248 Human annexin V pr
2	1593	99.7	669	24	ABP56249 Modified annexin p
3	1580	98.9	318	20	AA113925 66T GFP variant/h
4	1575	98.6	319	16	AA175695 Rat annexin-V. Ra
5	1535	96.1	319	20	AA113924 66T GFP variant/h
6	1535	96.1	319	23	ABP57067 Mouse ischaemic co
7	1451.5	90.8	319	13	AA16276 CPG-I. Homo sapie
8	1451.5	90.8	319	14	AA16276 Calphobindin I (CP
9	1451.5	90.8	319	23	ABG32550 Human CPG-1 protei

10	1451.5	90.8	320	9	ABP80511
11	1451.5	90.8	320	10	ABP9953
12	1451.5	90.8	320	12	AA13082
13	1451.5	90.8	320	20	AA13923
14	1451.5	90.8	320	21	AA184788
15	1451.5	90.8	320	23	ABG31220
16	1448.5	90.6	320	10	ABP90053
17	1448.5	90.6	600	21	AA199930
18	1447.5	90.6	320	9	ABP8217
19	1446.5	90.5	319	13	AA126180
20	1445.5	90.5	320	9	ABP80242
21	1445.5	90.5	320	9	ABP80714
22	1445.5	90.5	320	12	AA11910
23	1442.5	90.3	327	22	ABP50863
24	1442.5	90.3	327	22	ABP50864
25	1442.5	90.3	327	22	ABP50865
26	1441.5	90.2	320	10	AA191363
27	1419.5	88.8	319	13	AA125718
28	921	57.6	321	20	AA13926
29	921	57.6	321	23	ABG96279
30	921	57.6	324	21	ABP4617
31	920	57.6	321	10	ABP9913
32	920	57.6	786	11	ABP03726
33	919	57.5	672	11	AA103725
34	919	57.5	675	24	ABU54621
35	904.5	56.6	320	21	AA184790
36	886	55.4	208	21	AA156393
37	870	54.4	503	14	AA134127
38	862	53.9	505	14	AA134128
39	858	53.7	505	20	AA107117
40	852	53.3	299	23	ABP63948
41	850	53.2	736	22	ABG19948
42	822.5	51.5	327	9	ABP80715
43	822.5	51.5	327	10	ABP1954
44	822.5	51.5	327	14	ABP3754
45	822.5	51.5	327	22	AA178665

ALIGNMENTS

RESULT 1
ABP56248
ID ABP56248 standard; Protein; 319 AA.
XX
AC ABP56248;
XX
DT 28-MAR-2003 (first entry)
XX
XX Human annexin V protein SEQ ID NO:3.
DE
XX
XX
KW Annexin; modified; thrombosis; annexin V; thrombolytic;
KW coronary thrombosis; overt cerebral thrombosis; arterial
KW transient cerebral ischemic attack; venous thrombosis.
XX
OS Homo sapiens.
XX
XX
XX WO200267857-A2.
XX
XX
XX 06-SEP-2002.
XX
XX
XX 21-FEB-2002; 2002WO-US05079.
XX
XX
XX 21-FEB-2001; 2001US-370402P.
XX
XX
XX 21-NOV-2001; 2001US-332582P.
XX
XX (SURRE-) SUBMITTED INC.
XX
XX
XX Allison A;
XX
XX
XX WPI; 2003-129062/12.
XX
XX N-PDB; AB221925.
XX

Placental coagulat
Vascular anti-coag
PAP-I. Homo sapie
66T GFP variant/h
Amino acid sequenc
Human annexin V, c
anticogulant Pp4
Annexin V/urokina
PAP-I isolated fro
CPB-I. Homo sapie
Sequence vascular
Sequence vascular
Vascular anticoagu
Modified human ann
Modified human ann
Human lipocortin-V
CPB-I. Homo sapie
66T GFP variant/h
Human ovarian can
Anticoagulative pr
Human placenta-der
Human placenta-der
Human NOVX polypep
Amino acid sequenc
Lung cancer associ
Annexin XI type I
Annexin XI type I
Lung cancer associ
Lung cancer associ
Novel human diagno
Sequence vascular
Vascular anti-coag
VAC-beta. Synthet
Human protein SEQ

QY 242 IRSIPAYLAETLYYAMKAGTDDHTLIRIVISRSEIDLFNIRKEFRKNFATSLYSMTKGD 301
 DB 256 IRSIPAYLAETLYYAMKAGTDDHTLIRIVISRSEIDLFNIRKEFRKNFATSLYSMTKGD 315
 QY 302 TSGDYKKAALLLCGGEDD 319
 DB 316 TSGDYKKAALLLCGGEDD 333

RESULT 3
 ID AAY13925 standard; protein; 318 AA.
 XX AAY13925;
 XX 13-JUL-1999 (first entry)
 XX 565T GFP variant/hannexin V protein.
 XX GFP; green fluorescent protein; annexin; fusion protein; apoptosis;
 KM fluorescent intensity; anionic phospholipid binding affinity;
 KM asymmetric distribution; plasma membrane phospholipid;
 KM apoptotic cell detection.
 XX Aequorea victoria.
 OS Homo sapiens.
 OS Synthetic.
 XX MO9919470-A2.
 XX 22-APR-1999.
 XX 09-OCT-1998; 98KO-US21444.
 XX 09-OCT-1997; 97US-0948276.
 XX (REGC) UNIV CALIFORNIA.
 XX Ernst JD;
 PI WPI; 1999-277634/23.
 DR Bifunctional fusion protein useful for the detection of apoptotic
 PT cells
 XX Claim 2; Page 17-18; 23pp; English.

CC This sequence represents an example of a protein of the invention.
 CC The proteins are bifunctional Aequorea victoria green fluorescent protein
 CC (GFP)-annexin fusion proteins, where the GFP and annexin moieties provide
 CC greater or equal fluorescent intensity and anionic phospholipid binding
 CC affinity, respectively, than do the corresponding unfused GFP and annexin
 CC proteins. An early manifestation of apoptosis is the loss of the
 CC asymmetric distribution of plasma membrane phospholipids, which results
 CC in exposure of anionic phospholipids on the extracellular leaflet of the
 CC plasma membrane. The GFP-annexin V fusion proteins are used for the
 CC detection of apoptotic cells by flow cytometry or fluorescent microscopy.
 CC The fusion proteins provide for homogeneously labelled annexin, with
 CC fluorescence properties that do not change upon binding membrane
 CC phospholipids, unlike prior art FITC-labelled annexins, where quenching
 CC of FITC-annexin V fluorescence by 40-50% occurs upon binding phospholipid
 CC membranes.
 CC Sequence 318 AA;
 XX SQ

Query Match 98.9%; Score 1580; DB 20; Length 318;
 Best Local Similarity 99.4%; Pred. No. 6.8e-133;
 Matches 316; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ALRGVTDFSGFDGADAEVLRKAMKGLGTDEDSIINLTLFASNAQRQIAEEFKTLPER 61
 DB 1 ALRGVTDFSGFDGADAEVLRKAMKGLGTDEDSIINLTLFASNAQRQIAEEFKTLPER 60

QY 62 DIVNDKSELNGKEFKLIVALKMPSRLYDAYELGKAKLGAGTDEKVLTEIIASRTPELR 121
 DB 61 DIVNDKSELNGKEFKLIVALKMPSRLYDAYELGKAKLGAGTDEKVLTEIIASRTPELR 120
 QY 122 AIKQAYEEBYGSLNEDDVPVSGTYQRMVYLQANRDPDTALDDAQVELDQAALFQAG 181
 DB 121 AIKQAYEEBYGSLNEDDVPVSGTYQRMVYLQANRDPDTALDDAQVELDQAALFQAG 180
 QY 182 ELKMGTDDEKFTTLIGTRSVSHLRVPDPKWTISGFOIETIDRETSNGLENLLAVKS 241
 DB 181 ELKMGTDDEKFTTLIGTRSVSHLRVPDPKWTISGFOIETIDRETSNGLENLLAVKS 240
 QY 242 IRSIPAYLAETLYYAMKAGTDDHTLIRIVISRSEIDLFNIRKEFRKNFATSLYSMTKGD 301
 DB 241 IRSIPAYLAETLYYAMKAGTDDHTLIRIVISRSEIDLFNIRKEFRKNFATSLYSMTKGD 300
 QY 302 TSGDYKKAALLLCGGEDD 319
 DB 301 TSGDYKKAALLLCGGEDD 318

RESULT 4
 ID AAR75695 standard; peptide; 319 AA.
 XX AAR75695;
 XX 21-JAN-1996 (first entry)
 XX Rat annexin-V.
 XX Amyloid precursor protein; APP; annexin-V; Alzheimer's disease;
 KM disease diagnosis; therapy; antibody.
 XX Rattus rattus.
 OS Key Location/Qualifiers
 XX FT Peptide 57..68
 XX FT Peptide 85..95
 XX FT Peptide 107..120
 XX FT Peptide 259..284
 XX BP655626-A1.
 XX 31-MAY-1995.
 XX 10-NOV-1994; 94EP-0308309.
 XX 10-NOV-1993; 93US-0149975.
 XX (MCLF-) MCLEAN HOSPITAL CORP.
 XX Honda T, Nixon R;
 PI WPI; 1995-195688/26.
 DR New peptide(s) associated with Alzheimer's disease - namely p33 and
 PT the amyloid precursor C2 fragment, useful for the prodn. of
 PT diagnostic antibodies
 XX Disclosure; Fig.9; 32pp; English.
 XX This amino acid sequence is contained within the 33 kDa protein
 CC (p33) sequence and the indicated peptides are produced following
 CC lysyl-endopeptidase cleavage of p33. Detection and quantification
 CC of this protein is therefore useful for diagnosing the disease.

Query Match 98.6%; Score 1575; DB 16; Length 319;
 Best Local Similarity 98.7%; Pred. No. 1.9e-132;
 Matches 315; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MALRGVTPSGFGADAEVLRKAMKGLGTEDESIINLTARSNAQROQIAEERKTLFG 60
 Db 1 WALRGVTPSGFGADAEVLRKAMKGLGTEDESIINLTARSNAQROQIAEERKTLFG 60
 QY 61 RDVNDKMSBELTGKFEKLIYALMKPSRLYDAVELKHAUKAGTDEKVLTEIIASRTPEEL 120
 Db 61 RDVNDKMSBELTGKFEKLIYALMKPSRLYDAVELKHAUKAGTDEKVLTEIIASRTPEEL 120
 QY 121 RAIKQAYEEYGSNLEDDVYDTSYQRMVLVLLQANRDPDTAIDDAQVELDAQALFOA 180
 Db 121 RAIKQAYEEYGSNLEDDVYDTSYQRMVLVLLQANRDPDTAIDDAQVELDAQALFOA 180
 QY 181 GELKMGTEDEKFTITLIGTRSVSHLRVFDKXMTISGFQIEETIDRETSGNLENTLLAVK 240
 Db 181 GELKMGTEDEKFTITLIGTRSVSHLRVFDKXMTISGFQIEETIDRETSGNLENTLLAVK 240
 QY 241 SIRSIPIYLAETLYYAMKAGTDDHTLIRIVSRSEIDLFNIRKEFRKNFATSLYSMTKG 300
 Db 241 SIRSIPIYLAETLYYAMKAGTDDHTLIRIVSRSEIDLFNIRKEFRKNFATSLYSMTKG 300
 QY 301 DTSGDYKKALLLLCGGEDD 319
 Db 301 DTSGDYKKALLLLCGGEDD 319

RESULT 5

AAV13924
 ID AAV13924 standard; protein; 319 AA.

XX AC AAV13924;
 DT 13-JUN-1999 (first entry)
 DE S65T GFP variant/hannexin V protein.
 XX KW GFP; green fluorescent protein; annexin; fusion protein; apoptosis;
 KW fluorescent intensity; anionic phospholipid binding affinity;
 KW asymmetric distribution; plasma membrane phospholipid;
 KW apoptotic cell detection.
 XX OS Aequorea victoria.
 OS Homo sapiens.
 XX OS Synthetic.
 XX PN WO919470-A2.
 XX PD 22-APR-1999.
 XX PF 09-OCT-1998; 98WO-US21444.
 XX PR 09-OCT-1997; 97US-0948276.
 XX PA (REGC) UNIV CALIFORNIA.
 XX PI Ernst JD;
 XX DR WPI; 1999-277634/23.
 XX PT Bifunctional fusion protein useful for the detection of apoptotic
 PT cells
 XX PS Claim 2; Page 15-17; 23pp; English.
 CC This sequence represents an example of a protein of the invention.
 CC The proteins are bifunctional Aequorea victoria green fluorescent protein
 CC (GFP)-annexin fusion proteins, where the GFP and annexin moieties provide
 CC greater or equal fluorescent intensity and anionic phospholipid binding
 CC affinity, respectively, than do the corresponding unfused GFP and annexin
 CC proteins. An early manifestation of apoptosis is the loss of the
 CC asymmetric distribution of plasma membrane phospholipids, which results
 CC in exposure of anionic phospholipids on the extracellular leaflet of the
 CC plasma membrane. The GFP-annexin V fusion proteins are used for the
 CC detection of apoptotic cells by flow cytometry or fluorescent microscopy.

CC The fusion proteins provide for homogeneously labelled annexin, with
 CC fluorescence properties that do not change upon binding membrane
 CC phospholipids, unlike prior art FITC-labelled annexins, where quenching
 CC of FITC-annexin V fluorescence by 40-50% occurs upon binding phospholipid
 CC membranes.
 XX
 SQ Sequence 319 AA;

Query Match 96.1%; Score 1535; DB 20; Length 319;
 Best Local Similarity 95.3%; Pred. No. 7,1e-129;
 Matches 304; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 MALRGVTPSGFGADAEVLRKAMKGLGTEDESIINLTARSNAQROQIAEERKTLFG 60
 Db 1 MALRGVTPSGFGADAEVLRKAMKGLGTEDESIINLTARSNAQROQIAEERKTLFG 60
 QY 61 RDVNDKMSBELTGKFEKLIYALMKPSRLYDAVELKHAUKAGTDEKVLTEIIASRTPEEL 120
 Db 61 RDVNDKMSBELTGKFEKLIYALMKPSRLYDAVELKHAUKAGTDEKVLTEIIASRTPEEL 120
 QY 121 RAIKQAYEEYGSNLEDDVYDTSYQRMVLVLLQANRDPDTAIDDAQVELDAQALFOA 180
 Db 121 RAIKQAYEEYGSNLEDDVYDTSYQRMVLVLLQANRDPDTAIDDAQVELDAQALFOA 180
 QY 181 GELKMGTEDEKFTITLIGTRSVSHLRVFDKXMTISGFQIEETIDRETSGNLENTLLAVK 240
 Db 181 GELKMGTEDEKFTITLIGTRSVSHLRVFDKXMTISGFQIEETIDRETSGNLENTLLAVK 240
 QY 241 SIRSIPIYLAETLYYAMKAGTDDHTLIRIVSRSEIDLFNIRKEFRKNFATSLYSMTKG 300
 Db 241 SIRSIPIYLAETLYYAMKAGTDDHTLIRIVSRSEIDLFNIRKEFRKNFATSLYSMTKG 300
 QY 301 DTSGDYKKALLLLCGGEDD 319
 Db 301 DTSGDYKKALLLLCGGEDD 319

RESULT 6

ABB57067
 ID ABB57067 standard; protein; 319 AA.

XX AC ABB57067;
 DT 07-MAR-2002 (first entry)
 DE Mouse ischaemic condition related protein sequence SEQ ID NO:136.
 XX KW Mouse; ischaemia; compressive ischaemia; occlusive ischaemia;
 KW vasoospastic ischaemia; ischaemic condition; ischaemic disease.
 XX OS Mus musculus.
 XX PN WO200189188-A2.
 XX PD 22-NOV-2001.
 XX PF 18-MAY-2001; 2001WO-JP04192.
 XX PR 18-MAY-2000; 2000JP-0145977.
 XX PA (UNIV-) UNIV NITHON SCHOOL JURIDICAL PERSON.
 XX PI Ishikawa K, Asai S, Takahashi Y, Nagata T, Ishii Y;
 XX DR N-PSDB; AB199289.
 XX PT Examining the ischemic condition (e.g. occlusive ischemia) by measuring
 XX expression levels of particular genes defined in the specification or
 XX by determining the expression profile of a gene group comprising these
 XX genes -
 XX PS Claim 2; Page 419-421; 2690pp; English.

XX The present invention describes a method for examining ischaemic
 CC conditions, comprising measuring the expression levels of particular
 CC genes (I) in a test sample or determining the expression profile of a
 CC gene group in the sample comprising genes selected from (I). The method
 CC is useful for examining the ischaemic condition (e.g. compressive
 CC ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring
 CC expression levels of particular genes (AB199202 to AB199912, encoding
 CC the protein sequences in AB197020 to AB197374) or by determining the
 CC expression profile of a gene group comprising these genes. The
 CC expression levels or expression profiles produced by these genes are
 CC used as an indicator when screening for ischaemic condition-improving
 CC drugs or therapeutics for ischaemic diseases. AB199913 and AB199914
 CC represent PCR primers for a mouse ischaemic condition related sequence,
 CC which are used in the exemplification of the present invention.

SQ Sequence 319 AA;

Query Match 96.1%; Score 1535; DB 23; Length 319;
 Best Local Similarity 95.3%; Pred. No. 7, 1e-129;
 Matches 304; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 MALRGVTDFSGFDGADAEVLRKAMKGLGTDEDSILNLLTARSNAQSQIAEEFKTLFG 60
 Db 1 MATRGVTDFPGPDGRADAEVLRKAMKGLGTDEDSILNLLTSRSNAQSQIEAGFKTLFG 60
 QY 61 RDLVNDKSELTKGFEKLVVAMKPSRLYDAVELKHAKLGAGTDEKVTETIIASRTPBEL 120
 Db 61 RDLVNDKSELTKGFEKLVVAMKPSRLYDAVELKHAKLGAGTDEKVTETIIASRTPBEL 120
 QY 121 RAIKQAYEEYSGNLEDDVVGDTSGYQGMVLVLLQANRPDPTAIDDAQVELDQAALFOA 180
 Db 121 SAIKQAYEEYSGNLEDDVVGDTSGYQGMVLVLLQANRPDPTAIDDAQVELDQAALFOA 180
 QY 181 GEIKMGDEKFTTIGTSVSHLRVPDKWMTISGFQIEETIDETSQNLQALLAVVK 240
 Db 181 GEIKMGDEKFTTIGTSVSHLRVPDKWMTISGFQIEETIDETSQNLQALLAVVK 240
 QY 241 SIRSIPAYLAETLYAMKAGTDHDLIRVIVSRSEIDLFNIRKFRKNFATSLYSMTKG 300
 Db 241 SIRSIPAYLAETLYAMKAGTDHDLIRVIVSRSEIDLFNIRKFRKNFATSLYSMTKG 300
 QY 301 DTSGDYKALLLLCGGEDD 319
 Db 301 DTSGDYKALLLLCGGEDD 319

RESULT 7

AA26276 AAR26276 standard; protein; 319 AA.

XX AC AAR26276;
 XX DT 10-MAR-2003 (updated)
 XX DT 04-FEB-1993 (first entry)
 XX DE CPB-I.
 XX KM CPB-I; stabilisation; frozen; molten; processed; activity.
 XX OS Homo sapiens.
 XX PN JP04198195-A.
 XX PD 17-JUL-1992.
 XX PF 28-NOV-1990; 90JP-0328286.
 XX PR 28-NOV-1990; 90JP-0328286.
 XX PA (KAGA) KAGAKU OYOBI KESSEI RYOHO.
 XX PA (KOMA) KOMA CO LTD.
 XX PT

DR WPI; 1992-288937/35.

XX Stabilisation of CPB-I for drug compsn. - by adding basic
 PT aminoacid selected from lysine, arginine and/or ornithine
 XX
 XX Disclosure: Page 2; 4pp; Japanese.

XX The sequence given is the amino acid sequence of CPB-I. CPB-I was
 CC used within a method which involved adding basic amino acids to it
 CC which resulted in its stabilisation. This lead to the production of
 CC CPB-I which keeps its activity when it is frozen, molten or has been
 CC processed by several procedures.
 CC (updated on 10-MAR-2003 to add missing OS field.)

SQ Sequence 319 AA;

Query Match 90.8%; Score 1451.5; DB 13; Length 319;
 Best Local Similarity 91.5%; Pred. No. 2, 1e-121;
 Matches 290; Conservative 12; Mismatches 14; Indels 1; Gaps 1;

QY 3 LRGTVDPSGFDGADAEVLRKAMKGLGTDEDSILNLLTARSNAQSQIAEEFKTLFG 62
 Db 4 LRGTVDPSGFDGADAEVLRKAMKGLGTDEDSILNLLTSRSNAQSQIEAGFKTLFG 63
 QY 63 LVNDKSELTKGFEKLVVAMKPSRLYDAVELKHAKLGAGTDEKVTETIIASRTPBEL 122
 Db 64 LVNDKSELTKGFEKLVVAMKPSRLYDAVELKHAKLGAGTDEKVTETIIASRTPBEL 123
 QY 123 IKQAYEEYSGNLEDDVVGDTSGYQGMVLVLLQANRPDPTAIDDAQVELDQAALFOA 182
 Db 124 IKQAYEEYSGNLEDDVVGDTSGYQGMVLVLLQANRPDPTAIDDAQVELDQAALFOA 183
 QY 183 LKMGDEKFTTIGTSVSHLRVPDKWMTISGFQIEETIDETSQNLQALLAVVK 242
 Db 184 LKMGDEKFTTIGTSVSHLRVPDKWMTISGFQIEETIDETSQNLQALLAVVK 243
 QY 243 RSIPAYLAETLYAMKAGTDHDLIRVIVSRSEIDLFNIRKFRKNFATSLYSMTKG 302
 Db 244 RSIPAYLAETLYAMKAGTDHDLIRVIVSRSEIDLFNIRKFRKNFATSLYSMTKG 303
 QY 303 SGGDYKALLLLCGGEDD 319
 Db 304 SGGDYKALLLLC-GEED 319

RESULT 8

AA41021 AAR41021 standard; protein; 319 AA.

XX AC AAR41021;
 XX DT 29-MAR-1994 (first entry)
 XX DE Calphobindin I (CPB-I).
 XX KM Calphobindin I; CPB-I; Protein kinase C; PKC; inhibition; tumour.
 XX OS Homo sapiens.
 XX PN JP05213769-A.
 XX PD 24-AUG-1993.
 XX PF 04-FEB-1992; 92JP-0019032.
 XX PR 04-FEB-1992; 92JP-0019032.
 XX PA (KOMA) KOMA CO LTD.
 XX PA (KAGA-) ZH KAGAKU OYOBI KESSEN RYOHO KENKUTISHO.
 XX DR WPI; 1993-299558/38.
 XX PT Protein kinase C inhibitor effective against malignant tumours -

PT contg. (opt. recombinant) calphobindin I
 XX
 PS Claim 1; Page 2-3; 6pp; Japanese.
 XX
 CC Calphobindin I (CPB-I) or recombinant calphobindin I (r-CPB-I)
 CC inhibits protein kinase C (PKC) and is useful in the treatment of
 CC malignant tumours caused by abnormal activation of PKC. CPB-I is
 CC extracted from human or animal organs and may be applied
 CC intravenously, orally, intramuscularly, percutaneously or rectally.
 XX
 SQ Sequence 319 AA;
 Query Match 90.8%; Score 1451.5; DB 14; Length 319;
 Best Local Similarity 91.5%; Pred. No. 2.1e-121;
 Matches 290; Conservative 12; Mismatches 14; Indels 1; Gaps 1;
 QY 3 LRGYTDFSGFDGRADAEVLRKAMKGLGTDEDSILNLLTARSNAQRCQIAEFKTLFGRD 62
 DB 4 LRGYTDFSGFDGRADAEVLRKAMKGLGTDEDSILNLLTARSNAQRCQISAAFKTLFGRD 63
 QY 63 LVNDKSELTKGFEKLIYALMKPSRLYDAYELKXAKLGAGTDEKVTETIIASRPEELRA 122
 DB 64 LDDDKSELTKGFEKLIYALMKPSRLYDAYELKXAKLGAGTNEKVLTEIIASRPEELRA 123
 QY 123 IKQAYEEYGSNLEDDVVDGTSQYQRMVLVLLQANRPDPAIDDAQVELDAQALFQAGE 182
 DB 124 IKQAYEEYGSNLEDDVVDGTSQYQRMVLVLLQANRPDPAIDDAQVELDAQALFQAGE 183
 QY 183 LKMGTEBEKFTITLGRSVSHLRVPDKYMTISGFIETIDRETSNLEMLLAVVXSI 242
 DB 184 LKMGTEBEKFTITLGRSVSHLRVPDKYMTISGFIETIDRETSNLEMLLAVVXSI 243
 QY 243 RSIPAYIAETLYAMKAGTDDHTLIRIVSRSEIDLNFIRKEFRKNFATSIYSMTIKGDT 302
 DB 244 RSIPAYIAETLYAMKAGTDDHTLIRIVSRSEIDLNFIRKEFRKNFATSIYSMTIKGDT 303
 QY 303 SGDYKXALLLCGGEDD 319
 DB 304 SGDYKXALLLC-GEED 319

RESULT 9
 ABG32550
 ID ABG32550 standard; protein; 319 AA.
 AC ABG32550;
 XX
 DT 29-NOV-2002 (first entry)
 XX
 DE Human CPB-1 protein.
 XX
 KW Human; CPB-I; eye drop; ophthalmological; anexin V; corneal disease;
 KW calcium/phospholipid binding protein; polyhydric alcohol.
 XX
 OS Homo sapiens.
 XX
 PN WO200267977-A1.
 XX
 PD 06-SEP-2002.
 XX
 PF 21-FEB-2002; 2002WO-JP01563.
 XX
 PR 26-FEB-2001; 2001JP-0050297.
 XX
 PA (KOWA) KOMA CO LTD.
 PA (KAGA) CHEMO-SERO-THERAPEUTIC RES INST.
 XX
 PI Naruse H, Sano M, Shinoda Y, Inagi T;
 XX
 DR WPI; 2002-674988/72.
 XX
 PT Eye drops for treating e.g. corneal diseases, contain CPB-I and
 PT polyhydric alcohol with specific carbonyl value, without unpleasant

PT irritation upon dropping but with satisfactory long-term storability
 XX
 PS Disclosure; Page 13-14; 16pp; Japanese.
 XX
 CC The invention relates to eye drops contain CPB-I (anexin V) and a
 CC polyhydric alcohol having a carbonyl value of not more than
 CC 5mg/ml. The eye drops are for treating e.g. corneal diseases.
 CC Such eye drops are without unpleasant irritation upon dropping but with
 CC satisfactory long-term storage stability. The present sequence is
 CC the human CPB-I (calcium/phospholipid binding) protein.
 XX
 SQ Sequence 319 AA;
 Query Match 90.8%; Score 1451.5; DB 23; Length 319;
 Best Local Similarity 91.5%; Pred. No. 2.1e-121;
 Matches 290; Conservative 12; Mismatches 14; Indels 1; Gaps 1;
 QY 3 LRGYTDFSGFDGRADAEVLRKAMKGLGTDEDSILNLLTARSNAQRCQIAEFKTLFGRD 62
 DB 4 LRGYTDFSGFDGRADAEVLRKAMKGLGTDEDSILNLLTARSNAQRCQISAAFKTLFGRD 63
 QY 63 LVNDKSELTKGFEKLIYALMKPSRLYDAYELKXAKLGAGTDEKVTETIIASRPEELRA 122
 DB 64 LDDDKSELTKGFEKLIYALMKPSRLYDAYELKXAKLGAGTNEKVLTEIIASRPEELRA 123
 QY 123 IKQAYEEYGSNLEDDVVDGTSQYQRMVLVLLQANRPDPAIDDAQVELDAQALFQAGE 182
 DB 124 IKQAYEEYGSNLEDDVVDGTSQYQRMVLVLLQANRPDPAIDDAQVELDAQALFQAGE 183
 QY 183 LKMGTEBEKFTITLGRSVSHLRVPDKYMTISGFIETIDRETSNLEMLLAVVXSI 242
 DB 184 LKMGTEBEKFTITLGRSVSHLRVPDKYMTISGFIETIDRETSNLEMLLAVVXSI 243
 QY 243 RSIPAYIAETLYAMKAGTDDHTLIRIVSRSEIDLNFIRKEFRKNFATSIYSMTIKGDT 302
 DB 244 RSIPAYIAETLYAMKAGTDDHTLIRIVSRSEIDLNFIRKEFRKNFATSIYSMTIKGDT 303
 QY 303 SGDYKXALLLCGGEDD 319
 DB 304 SGDYKXALLLC-GEED 319

RESULT 10
 AAP80511
 ID AAP80511 standard; protein; 320 AA.
 AC AAP80511;
 XX
 DT 25-MAR-2003 (updated)
 DT 10-MAR-2003 (updated)
 DT 12-NOV-1990 (first entry)
 XX
 DE Placental coagulation inhibitor.
 XX
 KW Placental coagulation inhibitor; disseminated vascular coagulation;
 KW thrombosis.
 XX
 OS Homo sapiens.
 XX
 PN EP279459-A.
 PN JP03219875-A.
 XX
 PD 24-AUG-1988.
 XX
 PF 19-FEB-1988; 88EP-0102468.
 XX
 PR 20-FEB-1987; 87JP-0037227.
 PR 23-JUL-1987; 87JP-0184428.
 XX
 PA (KOWA) KOMA CO LTD.
 PA Sano Y, Iwasaki A, Suda M;
 XX
 PI

DR WPI, 1988-236733/34.
 DR WPI, 1991-32910/45.
 DR N-PSDB; AAN8113.
 XX
 PT Recombinant placental coagulation inhibitor - useful for the prevention
 PT and treatment of thromboses or disseminated intra-vascular coagulation.
 XX
 PS Disclosure, Page 2, 7pp; English.
 XX
 CC This polypeptide exhibits strong anticoagulant activities and is useful
 CC for the treatment and prevention of e.g. thrombosis or disseminated
 CC intravascular coagulation in the brain, heart and peripheral blood
 CC vessels, such as cerebral and myocardial infarction. It has no
 CC antigenicity against man and can be produced in large amounts using
 CC recombinant methods.
 CC (Updated on 10-MAR-2003 to add missing OS field.)
 CC (Updated on 25-MAR-2003 to correct PF field.)
 CC (Updated on 25-MAR-2003 to correct PR field.)
 CC (Updated on 25-MAR-2003 to correct PA field.)
 XX
 SQ Sequence 320 AA;
 Query Match 90.8%; Score 1451.5; DB 9; Length 320;
 Best Local Similarity 91.5%; Pred. No. 2.1e-121;
 Matches 290; Conservative 12; Mismatches 14; Indels 1; Gaps 1;
 QY 3 LRGTVTDFSGFGRADAEVLRKAMKGLGTDSESLNLTARSNAQROQIAEEFTLFGRD 62
 DB 5 LRGTVTDFSGFGRADAEVLRKAMKGLGTDSESLNLTARSNAQROQIAEEFTLFGRD 64
 QY 63 LVNDKSELTGKFEKLIYALMKPSRLYDAVELKAKLGAQDEKVTETIIASRTPEELRA 122
 DB 65 LDDDKSELTGKFEKLIYALMKPSRLYDAVELKAKLGAQDEKVTETIIASRTPEELRA 124
 QY 123 IKQAYEEYGSNLEDVVGDTSGYYQRMVLVLLQANRDPDAIDDAQVELDAQALFQAGE 182
 DB 125 IKQAYEEYGSNLEDVVGDTSGYYQRMVLVLLQANRDPDAIDDAQVELDAQALFQAGE 184
 QY 183 LKMGTDDEKFTITLGRSVSHLRVDFKXMTISGQIEETIDRETSGNLEMLLAAYKSI 242
 DB 185 LKMGTDDEKFTITLGRSVSHLRVDFKXMTISGQIEETIDRETSGNLEMLLAAYKSI 244
 QY 243 RSIPIYLAETLYYAMKAGTDHLLIRVYSRSEIDLFNIRKEPKNFATSLYSMTKGD 302
 DB 245 RSIPIYLAETLYYAMKAGTDHLLIRVYSRSEIDLFNIRKEPKNFATSLYSMTKGD 304
 QY 303 SGDYKXKALLLCCGEDD 319
 DB 305 SGDYKXKALLLCCGEDD 320
 RESULT 11
 AAR1953
 ID AAR1953 standard; protein; 320 AA.
 XX
 AC AAR1953;
 XX
 DT 25-MAR-2003 (updated)
 DT 10-MAR-2003 (updated)
 DT 30-JUL-1989 (first entry)
 XX
 DS Vascular anti-coagulating protein-alpha.
 XX
 KM Vascular anti-coagulating proteins; hybridomas; B-cells; myelomas.
 XX
 OS Chimeric - Homo sapiens.
 OS Chimeric - Mus musculus.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..320
 XX /product=VAC-alpha protein
 PN DE3810331-A.

XX
 PD 05-OCT-1989.
 XX
 PF 26-MAR-1988; 88DE-3810331.
 XX
 PR 26-MAR-1988; 88DE-3810331.
 XX
 PA (BOEH) BOEHRINGER INGELHEIM.
 XX
 PI Gunther A;
 XX
 DR WPI, 1989-293724/41.
 DR N-PSDB; AAN91353.
 XX
 PT Monoclonal antibodies to vascular anti-coagulating proteins - and
 PT hybridomas producing such antibodies.
 XX
 PS Disclosure, fig 1, 11pp; German.
 XX
 CC This vascular anti-coagulating protein (VAC)-alpha is used in the
 CC preparation of monoclonal antibodies (VABs). The VAC-alpha is injected
 CC into a host animal, in conjugation with eg keyhole limpet haemocyanin,
 CC and the B-cells from immunised hosts are then fused with myeloma cells.
 CC The resultant hybridomas (VAA-8 and VAA-9) produce Abs specific to VAC-
 CC alpha. Abs can be used as immunoassay reagents to detect VAC proteins,
 CC as affinity ligands for protein purification, and as medicaments for binding
 CC and/or neutralising VAC proteins in vivo. See also AAN91354 and
 CC EP-181465.
 CC (Updated on 10-MAR-2003 to add missing OS field.)
 CC (Updated on 25-MAR-2003 to correct PA field.)
 XX
 SQ Sequence 320 AA;
 Query Match 90.8%; Score 1451.5; DB 10; Length 320;
 Best Local Similarity 91.5%; Pred. No. 2.1e-121;
 Matches 290; Conservative 12; Mismatches 14; Indels 1; Gaps 1;
 QY 3 LRGTVDPSGFGADAEVLRKAMKGLGTDSESLNLTARSNAQROQIAEEFTLFGRD 62
 DB 5 LRGTVDPSGFGADAEVLRKAMKGLGTDSESLNLTARSNAQROQIAEEFTLFGRD 64
 QY 63 LVNDKSELTGKFEKLIYALMKPSRLYDAVELKAKLGAQDEKVTETIIASRTPEELRA 122
 DB 65 LDDDKSELTGKFEKLIYALMKPSRLYDAVELKAKLGAQDEKVTETIIASRTPEELRA 124
 QY 123 IKQAYEEYGSNLEDVVGDTSGYYQRMVLVLLQANRDPDAIDDAQVELDAQALFQAGE 182
 DB 125 IKQAYEEYGSNLEDVVGDTSGYYQRMVLVLLQANRDPDAIDDAQVELDAQALFQAGE 184
 QY 183 LKMGTDDEKFTITLGRSVSHLRVDFKXMTISGQIEETIDRETSGNLEMLLAAYKSI 242
 DB 185 LKMGTDDEKFTITLGRSVSHLRVDFKXMTISGQIEETIDRETSGNLEMLLAAYKSI 244
 QY 243 RSIPIYLAETLYYAMKAGTDHLLIRVYSRSEIDLFNIRKEPKNFATSLYSMTKGD 302
 DB 245 RSIPIYLAETLYYAMKAGTDHLLIRVYSRSEIDLFNIRKEPKNFATSLYSMTKGD 304
 QY 303 SGDYKXKALLLCCGEDD 319
 DB 305 SGDYKXKALLLCCGEDD 320
 RESULT 12
 AAR13082
 ID AAR13082 standard; Protein; 320 AA.
 XX
 AC AAR13082;
 XX
 DT 25-MAR-2003 (updated)
 DT 30-SEP-1991 (first entry)
 XX
 DE PAP-I.
 XX

KW		Phospholipid; binding protein; lipocortin, domain; vitamin K; PBP;
KV		gla-domain; VKP.
XX		
XX		Homo sapiens.
OS		
XX		
PN		MO9109953-A.
XX		
PD		11-JUL-1991.
XX		
PF		13-DEC-1990; 90WO-US07335.
XX		
ER		29-DEC-1989; 89US-0459082.
XX		
FA		(Zymo) ZYMOGENETICS INC.
XX		
P1		Foster DC,
XX		
DR		WPI; 1991-2222905/30.
DR		N-PSDB; AAQ12679.
XX		
PT		Recombinant prodn. of hybrid phospholipid-binding proteins -
PT		comprising lipocortin phospholipid-binding domain and
XX		vitamin K-dependent protein
XX		
PS		Disclosure; Fig 7; 57pp; English.
XX		
CC		This sequence, or a fragment of it, is used in the construction of
CC		hybrid phospholipid-binding proteins (PBP) comprising at least one
CC		lipocortin phospholipid binding domain (PBD), e.g. of PAP-I, joined
CC		to a gla-domainless vitamin K-dependent protein, e.g. protein C or
CC		activated protein C. See AAQ12680-81 for such examples.
CC		See also AAQ12678-81.
CC		(Updated on 25-MAR-2003 to correct PA field.)
XX		
SO		Sequence 320 AA;
XX		
Query Match		90.8%; Score 1451.5; DB 12; Length 320;
Best Local Similarity		91.5%; Pred. No. 2,1e-121;
Matches 290; Conservative 12; Mismatches 14; Indels 1; Gaps 1		
DQ		3 LRGTVVDGSGFDGRADAEVLKAKMKGLTGDEDSILNLTARSNQROOIAEPEFTLFGRD 62
Db		5 LRGTIVDFPEFDRADAETLRKMKGLGTDESILTITLSRNQROEISAKTILFGRD 64
QY		63 LVNDMSSELTGKEFKLIVALMKPRSLDYAEIKPAKAGTDEKYLTEITIASRTPEELRA 122
Db		65 LLDDLKSELTGKEFKLIVALMKPRSLDYAEIKPALKAGTNEKYLTEITIASRTPEELRA 124
QY		123 IKOAYEEBYSNLDEDVDGTSGYQRMLVLLQANRPDPALIDAQVELDAQLFOAGE 182
Db		125 IKQYEEBYSNLDEDVDGTSGYQRMLVLLQANRPDAGIDEAQVEDQAQLFOAGE 184
QY		183 LKMGTDBEKKITTLTGRSVSHLRKFVDMKTSGCFQLETTIDRETSGNLENLLAVYKS1 242
Db		185 LKMGTDBEKKITTFGRSVSHLRKFVDMKTSGQILETTIDRETSGNLQLLAVYKS1 244
QY		243 RSIIPAYLAETLYAMKAGATDHTLIRLVISSEIDLINIKKERKKAFLSVMIGDT 302
Db		245 RSIIPAYLAETLYAMKAGATDHTLIRVVVSSEIDLINIKKERKKAFLSVMIGDT 304
QY		303 SGDYKKALLLLCGGEDD 319
Db		305 SGGDKKALLLLC-GEDD 320
RESULT 13		
ID	AAV13923	standard; protein; 320 AA.
XX	AAV13923;	
XX		
DT	13-JUL-1999	(first entry)
XX		

S65T GFP variant/AAnnexin V protein.

GFP; green fluorescent protein; annexin, fusion protein; apoptosis;
fluorescent intensity; anionic phospholipid binding affinity;
asymmetric distribution; plasma membrane phospholipid;
apoptotic cell detection.

Aequorea victoria.
Homo sapiens.
Synthetic.

M09J9I470-A2.
WU
XX XX
PN PN
FN FN
XX XX
FF FF
PP PP
RR RR
PA PA
FA FA
XX XX
PI PI
Ernst JD,
XX XX
DR DR
WP1; 1999-277634/23.
FT FT
cells

Bifunctional fusion protein useful for the detection of apoptotic
claim 2; Page 14-15; 23pp; English.

This sequence represents an example of a protein of the invention.
The proteins are bifunctional Aequorea victoria green fluorescent protein
(GFP)-annexin fusion proteins, where the GFP and annexin moieties provide
greater or equal fluorescent intensity and anionic phospholipid binding
affinity, respectively, than do the corresponding unfused GFP and annexin
proteins. An early manifestation of apoptosis is the loss of the
asymetric distribution of plasma membrane phospholipids, which results
in exposure of anionic phospholipids on the extracellular leaflet of the
plasma membrane. The GFP-annexin V fusion proteins are used for the
detection of apoptotic cells by flow cytometry or fluorescent microscopy.
CC CC
CC CC
phospholipids, unlike prior art FITC-labelled annexin, with
FITC-annexin V fluorescence by 40-50% occurs upon binding phospholipid
membranes.

Sequence 320 AA;

Query Match 90.8%; Score 1451.5; DB 20; Length 320;
Best Local Similarity 91.5%; Pred. No. 2,1e-121;
Matches 299; Conservative 12; Mismatches 14; Indels 1; Gaps 1

LKGTVDSEGFDPGRDAEVLTKANKKGAGTGDEDSILNLTAFNSAQROQIAEEFKTLFGSD 62
DB 5 LRTVTDVFPGFPERADAETLRKKAMKGATGEESILTITRSNAOQEISAARLTFGRD 64
63 LVNDMSESLTGKFEXLIYALMKPESLYDAYELKAAXLAGATDEKVTEIIASRTPBELRA 122
:::|
65 LDDDLSELTLGFEKLITYALKKPRLDYAYLKAKALGAQTNEVKLTEIIASTPEBLTA 124
123 IKAIVBEEGSNLEDDVVGDTSGYQRMLVTLLCANRPDTAIDDAQVELLDQAQLQAQS 182
125 IKQVIEEEKSSLEDVVGDTSGYYQRMLVTLLQANRDPDAGIDEAQVEQDAQLFOAGE 184
183 LKNKGTOEKXFIITLGSRVSYLRFVPDKWTISGSFOJEETIDRETSGNLENLLLAVYSI 242
185 LKMGTDKEKFIITPGIRSVSHRKYPDKWMTISGFOJEETIDRETSNGNELLLAVYSI 244
243 RSTPATLAARTLYYANKKGAGTDHTLTRIVYSRSTDIFNRKSPFRKPFATLSYMSIKGP 302
Db 245 RSTPATLAARTLYYANKKGAGTDHTLTRIVWSRSEIDLFINRKEPRNFATLSYMSIKGP 304
303 SGDIYKCALILLGGEDD 319

Db 305 SGDYKALLLLC-GEED 320

RESULT 14
ID AAY84788 standard; peptide; 320 AA.
XX AAY84788;
XX 08-AUG-2000 (first entry)
XX Amino acid sequence of annexin V.
XX Annexin; phospholipid; antithrombotic; antitumor; antiinflammatory;
XX coating; thrombogenic biomaterial; labelling compound; negative charge.
XX Unidentified.
XX Key Location/Qualifiers
FT Domain 16..91 /note="domain 1"
XX FR284106-A1.
XX 07-APR-2000.
XX 02-OCT-1998; 98FR-0012366.
XX 02-OCT-1998; 98FR-0012366.
XX (COMS) COMMISSARIAT ENERGIE ATOMIQUE.
XX (UYPA-) UNIV CURIE PARIS VI P & M.
XX Sanson A, Rosso MF, Neumann JM, Cordier OF, Guerois R;
XX WPI; 2000-320664/28.
XX Chemical structure having affinity for phospholipid comprises chemical
PT platform comprising six residues supporting set of chemical functions
PT that are capable of binding to phospholipid
XX
XX Claim 13; Fig 6b; 63p; French.
XX The present sequence represents an annexin polypeptide. The domain of
CC annexin, which may be modified, is used to construct the chemical
CC compounds of the invention. The specification describes chemical
CC compounds which have an affinity for a phospholipid. The chemical
CC compounds comprise at least one chemical platform comprising six
CC residues supporting a set of chemical functions that are capable of
CC binding to the phospholipid and at least partly define the affinity
CC of the structure for the phospholipid. The compounds act as
CC phospholipid sequestrers. The compounds are useful for preparing
CC antithrombotic, antitumor and antiinflammatory medications, for
CC making coatings for thrombogenic biomaterials, and for preparing
CC labelling compounds useful for analysing and detecting negative
CC charges on cell surfaces and microvesicles in blood.
XX
SQ Sequence 320 AA;
Query March 90.84; Score 1451.5; DB 21; Length 320;
Best Local Similarity 91.54; Pred. No. 2.1e-121;
Matches 290; Conservative 12; Mismatches 14; Indels 1; Gaps 1;
QY 3 LRGTVDPSGFDGRADAEVLRKAMKGLGTDEDSILNLTARSNAQRQIAEEFKTLFGRD 62
Db 5 LRGTVDPSGFDGRADAEVLRKAMKGLGTDEDSILNLTARSNAQRQIAEEFKTLFGRD 64
QY 63 LNDNMSELTGKFEKLVIAIMKPSRLYDAVEIKHAKLGSGTEKVLTEIISRPEEIRA 122
Db 65 LNDNMSELTGKFEKLVIAIMKPSRLYDAVEIKHAKLGSGTEKVLTEIISRPEEIRA 124
QY 123 IKQAYEEYGSNLEDVVGDTSGYQRMVLVLLQANRPDRTAIDDAQVELDAQALFQAGE 182

Db 125 IKQAYEEYGSNLEDVVGDTSGYQRMVLVLLQANRPDRTAIDDAQVELDAQALFQAGE 184

QY 183 LKMGTEDEKFTITIGTSRVSRLRRVFDKMTISGFOIEETIDRETSGLNENLLAAVKS1 242
Db 165 LKMGTEDEKFTITIGTSRVSRLRRVFDKMTISGFOIEETIDRETSGLNENLLAAVKS1 244

QY 243 RSIPIVLAETLYAMKAGAGTDDHTLIRIVYSRSEIDFNIRKPRKQFASLSYMTKGT 302
Db 245 RSIPIVLAETLYAMKAGAGTDDHTLIRIVYSRSEIDFNIRKPRKQFASLSYMTKGT 304

QY 303 SGDYKALLLLC-GEED 319
Db 305 SGDYKALLLLC-GEED 320

RESULT 15
ID ABG31220 standard; Protein; 320 AA.
XX ABG31220;
XX 05-NOV-2002 (first entry)
XX Human annexin V, containing a delta RACK binding site.
XX Human; annexin V; delta RACK; delta protein kinase C; deltaPKC;
XX VI domain; vasotrophic; cerebroprotective; delatavi-1; delatavi-2; RACK;
XX pseudo-delta RACK; pseudo-delta receptor for activated C-kinase;
XX delatavi-1-5; PKC; protein kinase C; signal transduction; cell growth;
XX gene expression; ion channel activity; translocation; hypoxia; stroke;
XX ischaemic damage; creatine kinase.
XX Homo sapiens.
XX WO200257413-A2.
XX 25-JUL-2002.
XX 09-NOV-2001; 2001WO-US47556.
XX 18-JUN-2001; 2001US-262060P.
XX (STRD) UNIV LELAND STANFORD JUNIOR.
XX Mochly-Rosen D;
XX WPI; 2002-599715/64.
XX New delta protein kinase C peptide for reducing or enhancing damage to
PT cells or tissues exposed to ischemic or hypoxic event caused by stroke,
PT or for protecting tissue from damage due to ischemia
XX
XX Claim 45; Page 64-65; 65p; English.
XX The invention discloses peptides comprising delatavi-1, delatavi-2,
CC pseudo-delta receptors for activated C-kinase (RACK), delatavi-5 or their
CC derivatives or fragments. Protein kinase C (PKC) is a key enzyme in
CC signal transduction involved in a variety of cellular functions including
CC cell growth, regulation of gene expression and ion channel activity. The
CC localisation of different PKC isozymes to different areas of the cell in
CC turn appears due to binding of the activated isozymes to the specific
CC anchoring molecules (RACKs). Peptides that mimic either the PKC-binding
CC site on RACKs or the RACK-binding site on PKC are isozyme specific
CC translocation inhibitors of PKC. The disclosed peptides are useful in
CC activating or inhibiting translocation or function of delatavi-1, the
CC delatavi-5 agonists or antagonists are useful in reducing, enhancing or
CC protecting against damage to cells or tissues due to ischaemic or hypoxic
CC event caused by stroke. Acute administration of the peptides, conjugated
CC to a carrier peptide or a Tat-derived peptide, protected hearts against
CC ischaemic damage as shown by decreased release of creatine kinase. The
CC data indicate that in an intact heart, inhibition of delatavi-1 conferred
CC greater than 50% protection against ischaemic damage. The sequence

CC presented is human annexin V, which contains a delta RACK binding site.
XX Sequence 320 AA;

Query Match 90.8%; Score 1451.5; DB 23; Length 320;
Best Local Similarity 91.5%; Pred. No. 2,1e-121;
Matches 290; Conservative 12; Mismatches 14; Indels 1; Gaps 1;

```
QY 3 LRGTVDSSGPDGRADAVLRKAMKGLTDEDSIANLLTARSNAQRQIAEEFKTLFGRD 62
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 5 LRGTVDPPGFDERADAFTRKAMKGLTDEESITLTLTSRNAQRQIEISAAFKTLFGRD 64
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 63 LVNDKSELTKGFEKLIYALMKPSRLYDAVEIKAKLGAQTDEKVLTEIIASRPEELRA 122
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 65 LLDLKSSELTKGFEKLIYALMKPSRLYDAVEIKAKLGAQTNEKVLTEIIASRPEELRA 124
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 123 IKQAYEEBYGSLNEDDVVGGTSGYQRMVYLLQANRDPDAIDDAQVELDAQALFOAGE 182
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 125 IKQAYEEBYGSSLNEDDVVGGTSGYQRMVYLLQANRDPDAIDDAQVELDAQALFOAGE 184
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 183 LKMGIDEKFFITLITRSVSHLRVFDKWTISGFOIETIDRETSGNLENTLLAVYKSI 242
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 185 LKMGIDEKFFITLITRSVSHLRVFDKWTISGFOIETIDRETSGNLENTLLAVYKSI 244
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 243 RSIPAYLAETLYAMKAGTDDHTLIRIVSRSEIDLFINIRKEFRKRFATSLYSMTKSDT 302
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 245 RSIPAYLAETLYAMKAGTDDHTLIRIVSRSEIDLFINIRKEFRKRFATSLYSMTKSDT 304
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 303 SGDYKKAALLLCGGEDD 319
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 305 SGDYKKAALLLC-GEDD 320
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

Search completed: December 12, 2003, 14:50:02
Job time : 26.8613 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 12, 2003, 14:48:38 ; Search time 9.68623 Seconds
(without alignments)

1393.438 Million cell updates/sec

Title: PCT-US03-2432-3

Sequence: 1 MALRGVTDPSGFDGRADAB.....GDTSGDYKALLLLCGGEDD 319

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 4231058 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Issued Patents AA:*
1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfillseq1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1580	98.9	318	4	US-08-948-276-3
2	1575	98.6	319	2	US-08-149-975A-2
3	1535	96.1	319	4	US-08-948-276-2
4	1451.5	90.8	319	1	US-08-125-746-1
5	1451.5	90.8	320	1	US-08-125-746-3
6	1451.5	90.8	320	4	US-08-948-276-1
7	1451.5	90.8	320	6	5225537-4
8	1442.5	90.3	327	4	US-09-324-096A-2
9	1442.5	90.3	327	4	US-09-324-096A-4
10	1442.5	90.3	327	4	US-09-324-096A-6
11	921	57.6	321	4	US-08-948-276-4
12	916	57.3	319	3	US-08-536-136-14
13	870	54.4	503	3	US-08-536-136-2
14	870	54.4	505	3	US-08-536-136-4
15	785	49.1	323	4	US-08-948-276-5
16	760	47.6	466	3	US-08-536-136-13
17	622	38.9	346	4	US-08-948-276-6
18	374.5	23.4	316	4	US-09-335-932A-62
19	237.5	14.9	239	4	US-09-335-932A-65
20	221	13.8	184	4	US-09-335-932A-66
21	118	7.4	849	4	US-09-157-257-4
22	114	7.1	111	4	US-08-325-932A-63
23	111.5	7.0	1051	3	US-08-965-762-14
24	111.5	7.0	1051	4	US-09-911-927-14
25	111.5	7.0	1051	4	US-09-911-982-14
26	111.5	7.0	1051	4	US-09-911-888-14
27	109	6.8	701	3	US-08-923-511-2

28	109	6.8	701	4	US-09-416-874A-2	Sequence 2, Appli
29	105	6.6	73	4	US-09-325-932A-64	Sequence 64, Appli
30	105	6.6	365	4	US-09-149-476-696	Sequence 696, App
31	103.5	6.5	662	1	US-08-224-657-88	Sequence 88, Appl
32	103.5	6.5	662	4	US-09-354-138-88	Sequence 88, Appl
33	103	6.4	498	4	US-08-858-207A-310	Sequence 310, Appl
34	102	6.4	399	4	US-09-252-991A-22529	Sequence 22529, A
35	101.5	6.4	789	4	US-09-107-532A-6734	Sequence 6734, Ap
36	99.5	6.2	539	4	US-09-157-257-6	Sequence 6, Appli
37	99	6.2	611	4	US-09-252-991A-21158	Sequence 21158, A
38	98	6.1	501	4	US-09-157-257-8	Sequence 8, Appli
39	98	6.1	1098	3	US-08-923-992A-8	Sequence 8, Appli
40	97.5	6.1	395	4	US-09-107-532A-6955	Sequence 6955, Ap
41	97.5	6.1	421	4	US-09-252-991A-26478	Sequence 26478, A
42	97.5	6.1	457	4	US-09-134-001C-3838	Sequence 3838, Ap
43	95	5.9	1164	3	US-08-923-992A-2	Sequence 2, Appli
44	95	5.9	1164	3	US-08-923-992A-10	Sequence 10, Appl
45	94.5	5.9	441	4	US-09-328-352-5426	Sequence 5426, Ap

ALIGNMENTS

```
RESULT 1
US-08-948-276-3
; Sequence 3, Application US/08948276
; Patent No. 6511829
; GENERAL INFORMATION:
; APPLICANT: Ernst, Joel D.
; TITLE OF INVENTION: GFP-Annexin Fusion Proteins
; FILE REFERENCE: UCSF97-113
; CURRENT APPLICATION NUMBER: US/08/948,276
; CURRENT FILING DATE: 1997-10-09
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 318
; TYPE: PRT
; ORGANISM: rat
US-08-948-276-3

Query Match          98.9%; Score 1580; DB 4; Length 318;
Best Local Similarity 99.4%; Pred. No. 2.7e-149;
Matches 316; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 ALRGVTDPSGFDGRADABVLRKAMKGGTDEDTLNTLTARSNAQQAEEKTFGR 61
        |||
Db      1 ALRGVTDPSGFDGRADABVLRKAMKGGTDEDTLNTLTARSNAQQAEEKTFGR 60

QY      62 DVNDKSELTGKFEKLIYALMKPSRLYDAVELKXAKLGAAGTDEKVLTEIYASRTPBELR 121
        |||
Db      61 DVNDKSELTGKFEKLIYALMKPSRLYDAVELKXAKLGAAGTDEKVLTEIYASRTPBELR 120

QY      122 ATRQAEVEEYGSNLEDDVYGGTSGYQMLVYLQANRDPDTAIDDAQVEIDAAQLQAG 181
        |||
Db      121 ATRQAEVEEYGSNLEDDVYGGTSGYQMLVYLQANRDPDTAIDDAQVEIDAAQLQAG 180

QY      182 ELKMGDEKFTITIGTSVSHLRVPFKYMTISGFOIEFTIDRETSQNLNLLAVKS 241
        |||
Db      181 ELKMGDEKFTITIGTSVSHLRVPFKYMTISGFOIEFTIDRETSQNLNLLAVKS 240

QY      242 IRSIPYLAETIYVAMKAGTDDHTLIVIVSRSEIDFNIRKPRKNFATSLYSMTKGD 301
        |||
Db      241 IRSIPYLAETIYVAMKAGTDDHTLIVIVSRSEIDFNIRKPRKNFATSLYSMTKGD 300

QY      302 TSGDYKALLLLCGGEDD 319
        |||
Db      301 TSGDYKALLLLCGGEDD 318

RESULT 2
US-08-149-975A-2
; Sequence 2, Application US/08149975A
```

```

; Patent No. 5849600
; GENERAL INFORMATION:
; APPLICANT: Nixon, Ralph
; TITLE OF INVENTION: DIAGNOSTIC ASSAYS FOR ALZHEIMER'S
; TITLE OF INVENTION: DISEASE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/149,975A
; FILING DATE: 11-NOV-1993
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 04843/016001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 319 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-149-975A-2

```

```

Query Match          98.6%; Score 1575; DB 2; Length 319;
Best Local Similarity 98.7%; Pred. No. 8.5e-149;
Matches 315; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

```

```

QY 1 MALRGVTDPGSGFDGRADAEVLKRAMKGLGTDEDSILNLTARSNARQQAEEFTLFG 60
DB 1 MALRGVTDPGSGFDGRADAEVLKRAMKGLGTDEDSILNLTARSNARQQAEEFTLFG 60
QY 61 RDLVNDKSELTKGFEKLIYALMKPSRLYDAYELKHALKGAGTDEKVTLEIIASRTPEEL 120
DB 61 RDLVNDKSELTKGFEKLIYALMKPSRLYDAYELKHALKGAGTDEKVTLEIIASRTPEEL 120
QY 121 RAIKQAYEEYGSNLEDVVGDTSGYQRMVLVLLQANRPDPTAIDDAQVELDAQALFQA 180
DB 121 RAIKQAYEEYGSNLEDVVGDTSGYQRMVLVLLQANRPDPTAIDDAQVELDAQALFQA 180
QY 181 GELKMGTDDEKFTITLGRSVSHLRVDFDKMTISGFISETIDRETSNLEMLLAVVK 240
DB 181 GELKMGTDDEKFTITLGRSVSHLRVDFDKMTISGFISETIDRETSNLEMLLAVVK 240
QY 241 SIRSIPAYLAETLYYAMKAGTDDHTLIRVVSSEIDLNRKPEFRKPFATSLYSMIMG 300
DB 241 SIRSIPAYLAETLYYAMKAGTDDHTLIRVVSSEIDLNRKPEFRKPFATSLYSMIMG 300
QY 301 DTSGDYKXALLLLCGGEDD 319
DB 301 DTSGDYKXALLLLCGGEDD 319

```

```

RESULT 3
US-08-948-276-2
; Sequence 2, Application US/08948276
; Patent No. 6511829

```

```

; GENERAL INFORMATION:
; APPLICANT: Ernst, Joel D.
; TITLE OF INVENTION: GFP-Annexin Fusion Proteins
; FILE REFERENCE: US08/948,276
; CURRENT APPLICATION NUMBER: US/08/948,276
; CURRENT FILING DATE: 1997-10-09
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 319
; TYPE: PRT
; ORGANISM: mouse
; US-08-948-276-2

```

```

Query Match          96.1%; Score 1535; DB 4; Length 319;
Best Local Similarity 95.3%; Pred. No. 8.2e-145;
Matches 304; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

```

```

QY 1 MALRGVTDPGSGFDGRADAEVLKRAMKGLGTDEDSILNLTARSNARQQAEEFTLFG 60
DB 1 MALRGVTDPGSGFDGRADAEVLKRAMKGLGTDEDSILNLTARSNARQQAEEFTLFG 60
QY 61 RDLVNDKSELTKGFEKLIYALMKPSRLYDAYELKHALKGAGTDEKVTLEIIASRTPEEL 120
DB 61 RDLVNDKSELTKGFEKLIYALMKPSRLYDAYELKHALKGAGTDEKVTLEIIASRTPEEL 120
QY 121 RAIKQAYEEYGSNLEDVVGDTSGYQRMVLVLLQANRPDPTAIDDAQVELDAQALFQA 180
DB 121 RAIKQAYEEYGSNLEDVVGDTSGYQRMVLVLLQANRPDPTAIDDAQVELDAQALFQA 180
QY 181 GELKMGTDDEKFTITLGRSVSHLRVDFDKMTISGFISETIDRETSNLEMLLAVVK 240
DB 181 GELKMGTDDEKFTITLGRSVSHLRVDFDKMTISGFISETIDRETSNLEMLLAVVK 240
QY 241 SIRSIPAYLAETLYYAMKAGTDDHTLIRVVSSEIDLNRKPEFRKPFATSLYSMIMG 300
DB 241 SIRSIPAYLAETLYYAMKAGTDDHTLIRVVSSEIDLNRKPEFRKPFATSLYSMIMG 300
QY 301 DTSGDYKXALLLLCGGEDD 319
DB 301 DTSGDYKXALLLLCGGEDD 319

```

```

RESULT 4
US-08-125-746-1
; Sequence 1, Application US/08125746
; Patent No. 5531633
; GENERAL INFORMATION:
; APPLICANT: SAINO, YUSHI
; APPLICANT: IMASAKI, AKIO
; APPLICANT: SUDA, MAKOTO
; TITLE OF INVENTION: ANTICOAGULANT POLYPEPTIDE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/125,746
; FILING DATE: 24-SEP-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/807,623
; FILING DATE: 13-DEC-1991

```

PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 037227/1987
FILING DATE: 20-FEB-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 184428/1987
FILING DATE: 23-JUL-1987
ATTORNEY/AGENT INFORMATION:
NAME: Obion, No. 559163man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 80-074-0 DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 319 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-125-746-1

Query Match 90.8%; Score 1451.5; DB 1; Length 319;
Best Local Similarity 91.5%; Pred. No. 1.7e-136;
Matches 290; Conservative 12; Mismatches 14; Indels 1; Gaps 1;

QY 3 LRGTVDPSGFDGRADAELVRKAMKGLGTDSDSILNLTARSNARQOIAEEFKTLFGRD 62
DB 4 LRGTVDPSGFDGRADAELVRKAMKGLGTDSDSILNLTARSNARQOIAEEFKTLFGRD 63
QY 63 LVNDKSELTKGFEKILVALMKPSRLYDAVELKAKLGAGTDEKVLTIASRPEELRA 122
DB 64 LVDDKSELTKGFEKILVALMKPSRLYDAVELKAKLGAGTDEKVLTIASRPEELRA 123
QY 123 IKQAYEEYGSNLEDVVGDTSGYYQRMVLVLLQANDPDTAIDDAQVELDAQALFQAGE 182
DB 124 IKQAYEEYGSNLEDVVGDTSGYYQRMVLVLLQANDPDTAIDDAQVELDAQALFQAGE 183
QY 183 LKMGDDEKFTITLGRSVSHLRKVFQDKYMTISGFQIEETIDRETSGNLLENLLAAVXSI 242
DB 184 LKMGDDEKFTITLGRSVSHLRKVFQDKYMTISGFQIEETIDRETSGNLLENLLAAVXSI 243
QY 243 RSIPIVLAETLYYAMKAGTDDHTLIRVYRSSEIDLFINRKEFRKNFATSLYSMIKGD 302
DB 244 RSIPIVLAETLYYAMKAGTDDHTLIRVYRSSEIDLFINRKEFRKNFATSLYSMIKGD 303
QY 303 SGGYKXALLLCGGEDD 319
DB 304 SGGYKXALLLC-GEED 319

RESULT 5
US-08-125-746-3
Sequence 3, Application US/08125746
Patent No. 5591633
GENERAL INFORMATION:
APPLICANT: SAINO, YUSHI
APPLICANT: IMASAKI, AKIO
APPLICANT: SUDA, MAKOTO
TITLE OF INVENTION: ANTICOAGULANT POLYPEPTIDE
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBION, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/125,746
FILING DATE: 24-SEP-1993
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/807,623
FILING DATE: 13-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 037227/1987
FILING DATE: 20-FEB-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 184428/1987
FILING DATE: 23-JUL-1987
ATTORNEY/AGENT INFORMATION:
NAME: Obion, No. 559163man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 80-074-0 DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 320 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-125-746-3

Query Match 90.8%; Score 1451.5; DB 1; Length 320;
Best Local Similarity 91.5%; Pred. No. 1.7e-136;
Matches 290; Conservative 12; Mismatches 14; Indels 1; Gaps 1;

QY 3 LRGTVDPSGFDGRADAELVRKAMKGLGTDSDSILNLTARSNARQOIAEEFKTLFGRD 62
DB 5 LRGTVDPSGFDGRADAELVRKAMKGLGTDSDSILNLTARSNARQOIAEEFKTLFGRD 64
QY 63 LVNDKSELTKGFEKILVALMKPSRLYDAVELKAKLGAGTDEKVLTIASRPEELRA 122
DB 65 LVDDKSELTKGFEKILVALMKPSRLYDAVELKAKLGAGTDEKVLTIASRPEELRA 124
QY 123 IKQAYEEYGSNLEDVVGDTSGYYQRMVLVLLQANDPDTAIDDAQVELDAQALFQAGE 182
DB 125 IKQAYEEYGSNLEDVVGDTSGYYQRMVLVLLQANDPDTAIDDAQVELDAQALFQAGE 184
QY 183 LKMGDDEKFTITLGRSVSHLRKVFQDKYMTISGFQIEETIDRETSGNLLENLLAAVXSI 242
DB 185 LKMGDDEKFTITLGRSVSHLRKVFQDKYMTISGFQIEETIDRETSGNLLENLLAAVXSI 244
QY 243 RSIPIVLAETLYYAMKAGTDDHTLIRVYRSSEIDLFINRKEFRKNFATSLYSMIKGD 302
DB 245 RSIPIVLAETLYYAMKAGTDDHTLIRVYRSSEIDLFINRKEFRKNFATSLYSMIKGD 304
QY 303 SGGYKXALLLCGGEDD 319
DB 305 SGGYKXALLLC-GEED 320

RESULT 6
US-08-148-276-1
Sequence 1, Application US/08948276
Patent No. 6511829
GENERAL INFORMATION:
APPLICANT: Ernst, Joel D.
TITLE OF INVENTION: GFP-AnneXin Fusion Proteins
FILE REFERENCE: UCSF97-113
CURRENT APPLICATION NUMBER: US/08/948,276
CURRENT FILING DATE: 1997-10-09
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 320

TYPE: PRT
ORGANISM: human
US-08-948-276-1

Query Match 90.8%; Score 1451.5; DB 4; Length 320;
Best Local Similarity 91.5%; Pred. No. 1.7e-136;
Matches 290; Conservative 12; Mismatches 14; Indels 1; Gaps 1;

QY 3 LRGTVDPSGFDGADAEVLRKMKKGLGTDEDSILMLLTARSNAGQOIAEFKTLFGRD 62
DB 5 LRGTVDPSGFDGADAEVLRKMKKGLGTDEDSILMLLTARSNAGQOIAEFKTLFGRD 64
QY 63 LVNDKSELTKGFEKLIYALMKPSRLYDAYELKHAUKAGAGTDEKVLTEIISRTPEELRA 122
DB 65 LLDLKSSELTKGFEKLIYALMKPSRLYDAYELKHAUKAGAGTDEKVLTEIISRTPEELRA 124
QY 123 IKQAYEEYSGNLEDDVVGDTSGYQRMVLVLLQANRDPDAIDPAQVELDAQALFOAGE 182
DB 125 IKQAYEEYSGNLEDDVVGDTSGYQRMVLVLLQANRDPDAIDPAQVELDAQALFOAGE 184
QY 183 LKMGDEBEKFTITIGTRSVSHLRVFDKXMTISGFOIEETIDRETSGNLENLLAVVXSI 242
DB 185 LKMGDEBEKFTITIGTRSVSHLRVFDKXMTISGFOIEETIDRETSGNLENLLAVVXSI 244
QY 243 RSIPIAYLAETLYYAMKAGATDDHTLLIRVIVSRSEIDLFINRKEFRKNFATSLYSMTIKGDT 302
DB 245 RSIPIAYLAETLYYAMKAGATDDHTLLIRVIVSRSEIDLFINRKEFRKNFATSLYSMTIKGDT 304
QY 303 SGDYKALLLLCGEED 319
DB 305 SGDYKALLLLCGEED 320

RESULT 7
522537-4
Patent No. 522537
APPLICANT: FOSTER, DONALD
TITLE OF INVENTION: METHODS FOR PRODUCING HYBRID
PHOSPHOLIPID-BINDING PROTEINS
NUMBER OF SEQUENCES: 14
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/459, 082
FILING DATE: 29-DEC-1989
SEQ ID NO: 4
LENGTH: 320
522537-4

Query Match 90.8%; Score 1451.5; DB 6; Length 320;
Best Local Similarity 91.5%; Pred. No. 1.7e-136;
Matches 290; Conservative 12; Mismatches 14; Indels 1; Gaps 1;

QY 3 LRGTVDPSGFDGADAEVLRKMKKGLGTDEDSILMLLTARSNAGQOIAEFKTLFGRD 62
DB 5 LRGTVDPSGFDGADAEVLRKMKKGLGTDEDSILMLLTARSNAGQOIAEFKTLFGRD 64
QY 63 LVNDKSELTKGFEKLIYALMKPSRLYDAYELKHAUKAGAGTDEKVLTEIISRTPEELRA 122
DB 65 LLDLKSSELTKGFEKLIYALMKPSRLYDAYELKHAUKAGAGTDEKVLTEIISRTPEELRA 124
QY 123 IKQAYEEYSGNLEDDVVGDTSGYQRMVLVLLQANRDPDAIDPAQVELDAQALFOAGE 182
DB 125 IKQAYEEYSGNLEDDVVGDTSGYQRMVLVLLQANRDPDAIDPAQVELDAQALFOAGE 184
QY 183 LKMGDEBEKFTITIGTRSVSHLRVFDKXMTISGFOIEETIDRETSGNLENLLAVVXSI 242
DB 185 LKMGDEBEKFTITIGTRSVSHLRVFDKXMTISGFOIEETIDRETSGNLENLLAVVXSI 244
QY 243 RSIPIAYLAETLYYAMKAGATDDHTLLIRVIVSRSEIDLFINRKEFRKNFATSLYSMTIKGDT 302
DB 245 RSIPIAYLAETLYYAMKAGATDDHTLLIRVIVSRSEIDLFINRKEFRKNFATSLYSMTIKGDT 304
QY 303 SGDYKALLLLCGEED 319

DB 305 SGDYKALLLLCGEED 320

RESULT 8
US-09-324-096A-2
Sequence 2, Application US/09324096A
Patent No. 6323313
GENERAL INFORMATION:
APPLICANT: Tait, Jonathan
TITLE OF INVENTION: ANNEXIN DERIVATIVE WITH ENDOGENOUS CHELATION SITES
FILE REFERENCE: USFW-1-13841
CURRENT APPLICATION NUMBER: US/09/324, 096A
CURRENT FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 327
TYPE: PRT
ORGANISM: Homo sapiens
US-09-324-096A-2

Query Match 90.3%; Score 1442.5; DB 4; Length 327;
Best Local Similarity 91.2%; Pred. No. 1.4e-135;
Matches 289; Conservative 12; Mismatches 15; Indels 1; Gaps 1;

QY 3 LRGTVDPSGFDGADAEVLRKMKKGLGTDEDSILMLLTARSNAGQOIAEFKTLFGRD 62
DB 12 LRGTVDPSGFDGADAEVLRKMKKGLGTDEDSILMLLTARSNAGQOIAEFKTLFGRD 71
QY 63 LVNDKSELTKGFEKLIYALMKPSRLYDAYELKHAUKAGAGTDEKVLTEIISRTPEELRA 122
DB 72 LLDLKSSELTKGFEKLIYALMKPSRLYDAYELKHAUKAGAGTDEKVLTEIISRTPEELRA 131
QY 123 IKQAYEEYSGNLEDDVVGDTSGYQRMVLVLLQANRDPDAIDPAQVELDAQALFOAGE 182
DB 132 IKQAYEEYSGNLEDDVVGDTSGYQRMVLVLLQANRDPDAIDPAQVELDAQALFOAGE 191
QY 183 LKMGDEBEKFTITIGTRSVSHLRVFDKXMTISGFOIEETIDRETSGNLENLLAVVXSI 242
DB 192 LKMGDEBEKFTITIGTRSVSHLRVFDKXMTISGFOIEETIDRETSGNLENLLAVVXSI 251
QY 243 RSIPIAYLAETLYYAMKAGATDDHTLLIRVIVSRSEIDLFINRKEFRKNFATSLYSMTIKGDT 302
DB 252 RSIPIAYLAETLYYAMKAGATDDHTLLIRVIVSRSEIDLFINRKEFRKNFATSLYSMTIKGDT 311
QY 303 SGDYKALLLLCGEED 319
DB 312 SGDYKALLLLCGEED 327

RESULT 9
US-09-324-096A-4
Sequence 4, Application US/09324096A
Patent No. 6323313
GENERAL INFORMATION:
APPLICANT: Tait, Jonathan
TITLE OF INVENTION: ANNEXIN DERIVATIVE WITH ENDOGENOUS CHELATION SITES
FILE REFERENCE: USFW-1-13841
CURRENT APPLICATION NUMBER: US/09/324, 096A
CURRENT FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.0
SEQ ID NO 4
LENGTH: 327
TYPE: PRT
ORGANISM: Homo sapiens
US-09-324-096A-4

Query Match 90.3%; Score 1442.5; DB 4; Length 327;
Best Local Similarity 91.2%; Pred. No. 1.4e-135;
Matches 289; Conservative 12; Mismatches 15; Indels 1; Gaps 1;

QY 3 LRGTVDTSFGDGRADAEVLIRKAMKGLGTDDESIINLITARSNAQROQIAEFPKTLFGRD 62
 Db 12 LRGTVDTSFGDGRADAEVLIRKAMKGLGTDDESIINLITARSNAQROQIAEFPKTLFGRD 71
 QY 63 LVNDMSSELTGKFEKIVALKMPSRLYDAVELKHAHLKAGTDEKLTETIISRPPEELRA 122
 Db 72 LVNDMSSELTGKFEKIVALKMPSRLYDAVELKHAHLKAGTDEKLTETIISRPPEELRA 131
 QY 123 IKQAYEEYGSNLEDDVVGDTSGYQRMVLVLLQANRPDPTAIDDAQVELDAQALFOAGE 182
 Db 132 IKQAYEEYGSNLEDDVVGDTSGYQRMVLVLLQANRPDPTAIDDAQVELDAQALFOAGE 191
 QY 183 LKMGTDDEKFTITLIGRSVSHLRVDFDKMTISGFOIETTIDRETSGNLELLAVVXSI 242
 Db 192 LKMGTDDEKFTITLIGRSVSHLRVDFDKMTISGFOIETTIDRETSGNLELLAVVXSI 251
 QY 243 RSIIPAYLAETLYYAMKAGTDDHTLIRVIVSRSEIDLFNIRKEPKNFATSLYSMIKGD 302
 Db 252 RSIIPAYLAETLYYAMKAGTDDHTLIRVIVSRSEIDLFNIRKEPKNFATSLYSMIKGD 311
 QY 303 SGDYKALLLLCGGEDD 319
 Db 312 SGDYKALLLL--SGEDD 327

RESULT 10
 US-09-324-096A-6
 ; Sequence 6, Application US/09324096A
 ; Patent No. 6323313
 ; GENERAL INFORMATION:
 ; APPLICANT: Tait, Jonathan
 ; APPLICANT: Brown, David
 ; TITLE OF INVENTION: ANNEXIN DERIVATIVE WITH ENDOGENOUS CHELATION SITES
 ; FILE REFERENCE: US-09-324-096A
 ; CURRENT APPLICATION NUMBER: US/09/324, 096A
 ; CURRENT FILING DATE: 1999-06-01
 ; NUMBER OF SEQ ID NOS: 12
 ; SOFTWARE: Patent version 3.0
 ; SEQ ID NO 6
 ; LENGTH: 327
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-324-096A-6

Query Match 90.3%; Score 1442.5; DB 4; Length 327;
 Best Local Similarity 91.2%; Pred. No. 1.4e-135;
 Matches 289; Conservative 12; Mismatches 15; Indels 1; Gaps 1;

QY 3 LRGTVDTSFGDGRADAEVLIRKAMKGLGTDDESIINLITARSNAQROQIAEFPKTLFGRD 62
 Db 12 LRGTVDTSFGDGRADAEVLIRKAMKGLGTDDESIINLITARSNAQROQIAEFPKTLFGRD 71
 QY 63 LVNDMSSELTGKFEKIVALKMPSRLYDAVELKHAHLKAGTDEKLTETIISRPPEELRA 122
 Db 72 LVNDMSSELTGKFEKIVALKMPSRLYDAVELKHAHLKAGTDEKLTETIISRPPEELRA 131
 QY 123 IKQAYEEYGSNLEDDVVGDTSGYQRMVLVLLQANRPDPTAIDDAQVELDAQALFOAGE 182
 Db 132 IKQAYEEYGSNLEDDVVGDTSGYQRMVLVLLQANRPDPTAIDDAQVELDAQALFOAGE 191
 QY 183 LKMGTDDEKFTITLIGRSVSHLRVDFDKMTISGFOIETTIDRETSGNLELLAVVXSI 242
 Db 192 LKMGTDDEKFTITLIGRSVSHLRVDFDKMTISGFOIETTIDRETSGNLELLAVVXSI 251
 QY 243 RSIIPAYLAETLYYAMKAGTDDHTLIRVIVSRSEIDLFNIRKEPKNFATSLYSMIKGD 302
 Db 252 RSIIPAYLAETLYYAMKAGTDDHTLIRVIVSRSEIDLFNIRKEPKNFATSLYSMIKGD 311
 QY 303 SGDYKALLLLCGGEDD 319
 Db 312 SGDYKALLLL--SGEDD 327

RESULT 11
 US-08-948-276-4
 ; Sequence 4, Application US/08948276
 ; Patent No. 6511829
 ; GENERAL INFORMATION:
 ; APPLICANT: Ernst, Joel D.
 ; TITLE OF INVENTION: GFP-Annexin Fusion Proteins
 ; FILE REFERENCE: US/97-113
 ; CURRENT APPLICATION NUMBER: US/08/948, 276
 ; CURRENT FILING DATE: 1997-10-09
 ; NUMBER OF SEQ ID NOS: 6
 ; SOFTWARE: Patent ver. 2.0
 ; SEQ ID NO 4
 ; LENGTH: 321
 ; TYPE: PRT
 ; ORGANISM: human
 ; US-08-948-276-4

Query Match 57.6%; Score 921; DB 4; Length 321;
 Best Local Similarity 57.3%; Pred. No. 1.3e-83;
 Matches 180; Conservative 56; Mismatches 78; Indels 0; Gaps 0;

QY 5 GTVDFSGDGRADAEVLIRKAMKGLGTDDESIINLITARSNAQROQIAEFPKTLFGRD 64
 Db 8 GTVDFSGDGRADAEVLIRKAMKGLGTDDESIINLITARSNAQROQIAEFPKTLFGRD 67
 QY 65 NDMSSELTGKFEKIVALKMPSRLYDAVELKHAHLKAGTDEKLTETIISRPPEELRA 124
 Db 68 NDMSSELTGKFEKIVALKMPSRLYDAVELKHAHLKAGTDEKLTETIISRPPEELRA 127
 QY 125 IKQAYEEYGSNLEDDVVGDTSGYQRMVLVLLQANRPDPTAIDDAQVELDAQALFOAGE 184
 Db 128 IKQAYEEYGSNLEDDVVGDTSGYQRMVLVLLQANRPDPTAIDDAQVELDAQALFOAGE 187
 QY 185 LKMGTDDEKFTITLIGRSVSHLRVDFDKMTISGFOIETTIDRETSGNLELLAVVXSI 244
 Db 188 LKMGTDDEKFTITLIGRSVSHLRVDFDKMTISGFOIETTIDRETSGNLELLAVVXSI 247
 QY 245 RSIIPAYLAETLYYAMKAGTDDHTLIRVIVSRSEIDLFNIRKEPKNFATSLYSMIKGD 304
 Db 248 RSIIPAYLAETLYYAMKAGTDDHTLIRVIVSRSEIDLFNIRKEPKNFATSLYSMIKGD 307
 QY 305 DYKALLLLCGGEDD 318
 Db 308 DYKALLLL--CGGEDD 321

RESULT 12
 US-08-526-136-14
 ; Sequence 14, Application US/08526136
 ; Patent No. 6107089
 ; GENERAL INFORMATION:
 ; APPLICANT: Towle, Christine A. et al.
 ; TITLE OF INVENTION: ANNEXIN XI
 ; NUMBER OF SEQUENCES: 36
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Fish & Richardson
 ; STREET: 225 Franklin Street
 ; CITY: Boston
 ; STATE: Massachusetts
 ; COUNTRY: U.S.A.
 ; ZIP: 02110-2804
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 ; COMPUTER: IBM PS/2 Model 502 or 55SX
 ; OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
 ; SOFTWARE: WordPerfect (Version 5.0)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/526, 136
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:

```

/ APPLICATION NUMBER: US/08/214,036
/ FILING DATE:
/ APPLICATION NUMBER: 07/837,775
/ FILING DATE: February 13, 1992
/ APPLICATION NUMBER: 07/764,465
/ FILING DATE: September 23, 1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Clark, Paul T.
/ REGISTRATION NUMBER: 30,162
/ REFERENCE/DOCKET NUMBER: 00786/099001
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (617) 542-5070
/ TELEFAX: (617) 542-8906
/ TELEX: 200154
/ INFORMATION FOR SEQ ID NO: 14:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 319
/ TYPE: amino acid
/ STRANDEDNESS: N/A
/ TOPOLOGY: N/A
/
US-08-526-136-14

```

```

Query Match      57.3%; Score 916; DB 3; Length 319;
Best Local Similarity 57.3%; Pred. No. 4e-83;
Matches 180; Conservative 54; Mismatches 80; Indels 0; Gaps 0;

```

```

QY 5 GTVDFSGFGADAEVLRKAMKGLGTEDESIINLTARSNAQOQIAEEFKTLFGDL 64
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 6 GTVKAASGFNAEDQTLRKAMKGLGTEDEAIIVLAVRSQAQOELRTAYKTTIGRDL 65
QY 65 NDKSELTGKFEKTLVALMKPSRLYDAVELKAKLGAQTEKVTETIARSPEELRAI 124
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 66 DDKSELNSNFEQVILGNTPTVLDVQELRKAMKAGTDEGCILEIARSPEELRRI 125
QY 125 QAYEEYGSNLEDVVGDTSGYQSMVLVLLQANRDPDLADQVLELDAQALFOAGEL 184
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 126 QYVQIQYGSLEDDLRSDTSFMQKAVLSLSAGRDSNVIDDLAMQDQDIYKAGEKK 185
QY 185 WGTDEKFTTLIGTRSVSHLRVPDKRYTISGFOIETIDRETSNLENLLAVKXIRS 244
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 186 WGTDEVKFTLVCSNRNHLHVEFEYRIQKXIEQISKETSSEFDALLAIVKCMEN 245
QY 245 IYAVLAETLYAMKAGTDDHTLRVYSRSEIDLFINRKEFRNPFATSLYSMTKDGTS 304
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 246 KSAIYFAERLYAMKGLGTDITLIRVWVSRAIDMLDIRANFKLYGKSLYSPIKDGTS 305
QY 305 DYKALLLLCGGED 318
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 306 DYRKVLLILCGGD 319

```

```

RESULT 13
US-08-526-136-2
/ Sequence 2, Application US/08526136
/ Patent No. 6107089
/ GENERAL INFORMATION:
/ APPLICANT: Towle, Christine A. et al.
/ TITLE OF INVENTION: ANNEXIN XI
/ NUMBER OF SEQUENCES: 36
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Fish & Richardson
/ STREET: 225 Franklin Street
/ CITY: Boston
/ STATE: Massachusetts
/ COUNTRY: U.S.A.
/ ZIP: 02110-2804
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5" Diskette, 1.44 MB
/ COMPUTER: IBM PS/2 Model 502 or 55SX
/ OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
/ SOFTWARE: WordPerfect (Version 5.0)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/526,136

```

```

/ FILING DATE:
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/214,036
/ FILING DATE:
/ APPLICATION NUMBER: 07/837,775
/ FILING DATE: February 13, 1992
/ APPLICATION NUMBER: 07/764,465
/ FILING DATE: September 23, 1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Clark, Paul T.
/ REGISTRATION NUMBER: 30,162
/ REFERENCE/DOCKET NUMBER: 00786/099001
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (617) 542-5070
/ TELEFAX: (617) 542-8906
/ TELEX: 200154
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 503
/ TYPE: amino acid
/ TOPOLOGY: N/A
/
US-08-526-136-2

```

```

Query Match      54.4%; Score 870; DB 3; Length 503;
Best Local Similarity 55.6%; Pred. No. 3.1e-78;
Matches 175; Conservative 54; Mismatches 86; Indels 0; Gaps 0;

```

```

QY 4 RGTDFSGFGADAEVLRKAMKGLGTEDESIINLTARSNAQOQIAEEFKTLFGDL 63
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 189 RGTTFDASGFPDPRDLAEVLRKAMKGLGTEQAIIDLGSRKQOQILSKIVKGLD 248
QY 64 VNDKSELTGKFEKTLVALMKPSRLYDAVELKAKLGAQTEKVTETIARSPEELRAI 123
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 249 IKDKSELNSNFEKTLTALMKPVLFDAYEIKKAIKGAQTEACILEIARSNEHIEL 308
QY 124 KQAYEEYGSNLEDVVGDTSGYQSMVLVLLQANRDPDLADQVLELDAQALFOAGEL 183
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 309 NRKYKTFKLTLEAIRSDTSFGHFORLLISLQGRDESTNVDMTLVQDVELYAAEN 368
QY 184 KWTDEKFTTLIGTRSVSHLRVPDKRYTISGFOIETIDRETSNLENLLAVKXIRS 243
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 369 RLGTDESKFNALICSNRNHLVAVFNEYQRMGRDIKSIKEMSGDLEQGLAVKCLX 428
QY 244 SIPYLAETLYAMKAGTDDHTLRVYSRSEIDLFINRKEFRNPFATSLYSMTKDGTS 303
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 429 NTPAFFAERLYAMKAGTDDHTLRVWVSRAIDMLDIRANFKLYGKSLYHDTGTS 488
QY 304 GDYKALLLLCGGED 318
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 489 GDYRKILLIKICGND 503

```

```

RESULT 14
US-08-526-136-4
/ Sequence 4, Application US/08526136
/ Patent No. 6107089
/ GENERAL INFORMATION:
/ APPLICANT: Towle, Christine A. et al.
/ TITLE OF INVENTION: ANNEXIN XI
/ NUMBER OF SEQUENCES: 36
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Fish & Richardson
/ STREET: 225 Franklin Street
/ CITY: Boston
/ STATE: Massachusetts
/ COUNTRY: U.S.A.
/ ZIP: 02110-2804
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5" Diskette, 1.44 MB
/ COMPUTER: IBM PS/2 Model 502 or 55SX
/ OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
/ SOFTWARE: WordPerfect (Version 5.0)

```

```

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/526,136
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/214,036
FILING DATE:
APPLICATION NUMBER: 07/837,775
FILING DATE: February 13, 1992
APPLICATION NUMBER: 07/764,465
FILING DATE: September 23, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/099001
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 505
TYPE: amino acid
TOPOLOGY: N/A
US-08-526-136-4

Query Match      54.4%; Score 870; DB 3; Length 505;
Best Local Similarity 55.6%; Pred. No. 3.1e-78;
Matches 175; Conservative 54; Mismatches 86; Indels 0; Gaps 0;

QY 4 RGVITDFSGFDGRADAEVLRKAMKGLGTDEDSITNLLTASNAQRQIAEEFKTLFGDRL 63
DB 191 RGVITDASGFDPLRDAVLRKAMKGFDTBQALIDCLGSRSNKQROQILSLFKTAYGKDL 250

QY 64 VNMKSELTGKFEKLIYALMKPSRLYDAYELKAKLAGTDEKVLTEIIASRTPEELRAI 123
DB 251 IKDKSELSGNFEKTLTALMKTPVLPDAVEIKKAIKAGTDEACLEIIASRSNHEIREL 310

QY 124 KQAYEEVGSNLEDDVVDTSGYQRMVLVLLQANRPDTAIDDAQVELAQAQLFOAGEL 183
DB 311 NRVYKTFEKFTELEAIASDTSNGHFQRLISLSQGNPDESTVDMTVQSDVQELVYAGEN 370

QY 184 KMGTEDEKFTITLGRSVSHLRVFDKXMTISGFOIEETIDRETSNLENLLAVYSIR 243
DB 371 RLGTDESKFNALICSRRAHLVAVFNEYQMTGRDIEKISICREMSGDLEQGMILAVYKCLX 430

QY 244 SIPAYLAETLYYAMKAGTDHTLIRIVYSSRIDLFNIRKEFRKXNFATSLYSMTKSDTS 303
DB 431 NTPAFPAERLAKMKGAGTDORTLIRIMVSRSEIDLDIRAERYKLYGKSLYHDTIGDTS 490

QY 304 GDYKALLLLCGGED 318
DB 491 GDYRKILLKICGGND 505

RESULT 15
US-08-948-276-5
; Sequence 5, Application US/08948276
; Patent No. 6511829
; GENERAL INFORMATION:
; APPLICANT: Ernst, Joel D.
; TITLE OF INVENTION: GPP-Annexin Fusion Proteins
; FILE REFERENCE: US/97-113
; CURRENT APPLICATION NUMBER: US/08/948,276
; CURRENT FILING DATE: 1997-10-09
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 323
; TYPE: PRT
; ORGANISM: human
; US-08-948-276-5

```

```

Query Match      49.1%; Score 785; DB 4; Length 323;
Best Local Similarity 48.3%; Pred. No. 4.6e-70;
Matches 152; Conservative 68; Mismatches 95; Indels 0; Gaps 0;

QY 4 RGVITDFSGFDGRADAEVLRKAMKGLGTDEDSITNLLTASNAQRQIAEEFKTLFGDRL 63
DB 9 RGVITDYPFSSVDPAEAIQKAIKIGIDEKCLISILTERSNARQIIVKQAIYKEL 68

QY 64 VNMKSELTGKFEKLIYALMKPSRLYDAYELKAKLAGTDEKVLTEIIASRTPEELRAI 123
DB 69 KDLKGDLSGHEHLMVALTPPAVFDAKQKSKMKGAGTNEALTEIITRTSRQKDI 128

QY 124 KQAYEEVGSNLEDDVVDTSGYQRMVLVLLQANRPDTAIDDAQVELAQAQLFOAGEL 183
DB 129 SQAYTYTVKKSIGDDISSETSGDFKALLTLADGRDSSLKVDEHLAKQDAQILVYAGEN 188

QY 184 KMGTEDEKFTITLGRSVSHLRVFDKXMTISGFOIEETIDRETSNLENLLAVYSIR 243
DB 189 RMGTDEKFTTELCLRSFPQKLTPEDEVYRNISQKDIYDSIKGELSGHPEDLILAVNCR 248

QY 244 SIPAYLAETLYYAMKAGTDHTLIRIVYSSRIDLFNIRKEFRKXNFATSLYSMTKSDTS 303
DB 249 NTPAFPAERLAKMKGAGTDEFTLNIRIMVSRSEIDLDIRTEFKHGYSLYSAIKSDTS 308

QY 304 GDYKALLLLCGGED 318
DB 309 GDYEITLLKICGGDD 323

Search completed: December 12, 2003, 14:53:23
Job time : 10.6862 secs

```

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 12, 2003, 14:50:08 ; Search time 17.7581 Seconds
(without alignments)
3340.943 Million cell updates/sec

Title: PCT-US03-24332-3

Perfect score: 1598
Sequence: 1 MALRGVTVPFSGFDGRADAE.....GDTSGDYKALLLGGEDD 319

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 684280 seqs, 185983659 residues

Total number of hits satisfying chosen parameters: 684280

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Listing first 45 summaries

Published Applications_AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/2/pubpaa/US09B_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/2/pubpaa/US10C_NEW_PUB.pep:*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1598	100.0	319	12 US-10-080-370-3	Sequence 3, Appl1
2	1593	99.7	669	12 US-10-080-370-6	Sequence 6, Appl1
3	1451.5	90.8	320	14 US-10-007-761-72	Sequence 72, Appl1
4	1442.5	90.3	327	10 US-09-970-969-2	Sequence 2, Appl1
5	1442.5	90.3	327	10 US-09-970-969-4	Sequence 4, Appl1
6	1442.5	90.3	327	10 US-09-970-969-6	Sequence 6, Appl1
7	921	57.6	321	15 US-10-097-340-10	Sequence 10, Appl1
8	921	57.6	324	9 US-09-925-301-1062	Sequence 1062, Ap
9	886	55.4	208	9 US-09-925-302-731	Sequence 731, Ap
10	822.5	51.5	327	12 US-10-236-031B-18	Sequence 18, Appl
11	787	49.2	324	12 US-10-316-253-262	Sequence 262, Appl
12	785	49.1	323	15 US-10-205-823-34	Sequence 34, Appl
13	760	47.6	485	10 US-09-925-300-1664	Sequence 1664, Ap
14	695.5	43.5	339	10 US-09-974-298-91	Sequence 91, Appl
15	695.5	43.5	339	15 US-10-097-340-6	Sequence 6, Appl1

16	695.5	43.5	339	15 US-10-097-340-8	Sequence 8, Appl1
17	678	42.4	327	9 US-09-764-853-615	Sequence 615, App
18	675	42.2	332	11 US-09-764-881-110	Sequence 110, App
19	675	40.5	319	15 US-10-304-287-2	Sequence 2, Appl1
20	647.5	40.2	337	9 US-09-925-301-868	Sequence 868, App
21	622	38.9	373	10 US-09-919-172-39	Sequence 39, Appl
22	618	38.7	346	10 US-09-974-298-93	Sequence 93, Appl
23	618	38.7	346	10 US-09-974-298-93	Sequence 300, App
24	381.5	23.9	289	9 US-09-925-301-897	Sequence 897, App
25	376.5	23.6	316	15 US-10-219-220-260	Sequence 260, App
26	374.5	23.4	316	15 US-10-219-220-62	Sequence 62, Appl
27	315	19.7	158	9 US-09-925-297-479	Sequence 479, App
28	237.5	14.9	239	15 US-10-219-220-65	Sequence 65, Appl
29	223.5	14.0	319	12 US-10-259-165-56	Sequence 56, Appl
30	223.5	14.0	319	12 US-10-259-165-402	Sequence 402, App
31	221	13.8	184	15 US-10-219-220-66	Sequence 66, Appl
32	218	13.6	336	12 US-10-259-165-290	Sequence 290, App
33	139	8.7	82	9 US-09-925-301-1467	Sequence 1467, Ap
34	132	7.6	46	12 US-10-029-386-30160	Sequence 30160, A
35	114	7.1	111	15 US-10-219-220-63	Sequence 63, Appl
36	111.5	7.0	1051	10 US-09-911-888-13	Sequence 14, Appl
37	109	6.8	591	9 US-09-815-242-5837	Sequence 5837, A
38	109	6.8	701	9 US-09-815-242-13002	Sequence 13002, A
39	105	6.6	73	15 US-10-219-220-64	Sequence 64, Appl
40	105	6.6	365	11 US-09-809-391-696	Sequence 696, App
41	105	6.6	365	12 US-09-882-171-696	Sequence 696, App
42	103.5	6.5	662	11 US-09-951-051A-141	Sequence 141, App
43	99	6.2	617	9 US-09-815-242-13228	Sequence 13228, A
44	98.5	6.2	483	12 US-10-316-253-8	Sequence 8, Appl1
45	98	6.1	315	9 US-09-925-301-1053	Sequence 1053, Ap

ALIGNMENTS

RESULT 1
US-10-080-370-3
; Sequence 3, Application US/10080370
; Publication No. US20030166532A1
; GENERAL INFORMATION:
; APPLICANT: Allison, Anthony
; TITLE OF INVENTION: Modified Annexin Proteins and Methods for Preventing Thrombosis
; FILE REFERENCE: SURF.90
; CURRENT APPLICATION NUMBER: US/10/080.370
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/270,402
; PRIOR FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: 60/332,582
; PRIOR FILING DATE: 2001-11-21
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 319
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-080-370-3

Query Match 100.0%; Score 1598; DB 12; Length 319;
Best Local Similarity 100.0%; Pred. No. 3, 4e-142;
Matches 319; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MALRGVTVPFSGFDGRADAEVLRKAMKGLGDEDSINLLTASNMORQOIAEEFKTLFG	60
DB	1	MALRGVTVPFSGFDGRADAEVLRKAMKGLGDEDSINLLTASNMORQOIAEEFKTLFG	60
QY	61	RLVNDMKSSELTGKREKILVLMKPSRLDYAEIKKAKLGGTDEKYLTEIISRPPEEL	120
DB	61	RLVNDMKSSELTGKREKILVLMKPSRLDYAEIKKAKLGGTDEKYLTEIISRPPEEL	120
QY	121	RAIKAYEEFGNSINLEDDVVDVTGTYQRMVLVLLQNNRDPDPAIDAOVELDAQALFOA	180
DB	121	RAIKAYEEFGNSINLEDDVVDVTGTYQRMVLVLLQNNRDPDPAIDAOVELDAQALFOA	180

QY 181 GELKMGDEEKFITILGTRSVSHLRVYEDKMTISGFOIETTIDRETSQNLLELLAVYK 240
 DB 181 GELKMGDEEKFITILGTRSVSHLRVYEDKMTISGFOIETTIDRETSQNLLELLAVYK 240
 QY 241 SRSIPAYLAETLYYAMKAGTDHTLIRIVSRSEIDLFNIRKPKNFATSLYSMIKG 300
 DB 241 SRSIPAYLAETLYYAMKAGTDHTLIRIVSRSEIDLFNIRKPKNFATSLYSMIKG 300
 QY 301 DTSGDYKXALLLCCGEDD 319
 DB 301 DTSGDYKXALLLCCGEDD 319

RESULT 2

US-10-080-370-6
 ; Sequence 6, Application US/10080370
 ; Publication No. US20030166532A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Allison, Anthony
 ; TITLE OF INVENTION: Modified Annexin Proteins and Methods for Preventing Thrombosis
 ; FILE REFERENCE: SURR.90
 ; CURRENT APPLICATION NUMBER: US/10/080,370
 ; PRIOR FILING DATE: 2002-02-21
 ; PRIOR APPLICATION NUMBER: 60/270,402
 ; PRIOR FILING DATE: 2001-02-21
 ; PRIOR APPLICATION NUMBER: 60/332,582
 ; PRIOR FILING DATE: 2001-11-21
 ; NUMBER OF SEQ ID NOS: 9
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 6
 ; LENGTH: 669
 ; TYPE: PRT
 ; ORGANISM: Artificial sequence
 ; FEATURE:
 ; NAME/KEY: misc.feature
 ; LOCATION: (15)..(15)
 ; OTHER INFORMATION: The 'Xaa' at location 15 stands for Ser.
 ; NAME/KEY: misc.feature
 ; LOCATION: (334)..(334)
 ; OTHER INFORMATION: The 'Xaa' at location 334 stands for Lys, Asn, Arg, Ser, Thr, Ile
 ; OTHER INFORMATION: Tyr, Trp, Cys, or Phe.
 ; NAME/KEY: misc.feature
 ; LOCATION: (351)..(351)
 ; OTHER INFORMATION: The 'Xaa' at location 351 stands for Lys, Asn, Arg, Ser, Thr, Ile
 ; OTHER INFORMATION: Tyr, Trp, Cys, or Phe.
 ; NAME/KEY: misc.feature
 ; LOCATION: (45)..(45)
 ; OTHER INFORMATION: n = a, c, g, or t
 ; NAME/KEY: misc.feature
 ; LOCATION: (1000)..(1002)
 ; OTHER INFORMATION: n = a, c, g, or t
 ; NAME/KEY: misc.feature
 ; LOCATION: (1051)..(1053)
 ; OTHER INFORMATION: n = a, c, g, or t
 ; US-10-080-370-6

Query Match

Best Local Similarity 99.7%; Score 1593; DB 12; Length 669;
 Best Local Similarity 100.0%; Pred. No. 3e-141;
 Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ALRGVTFDSGFDGRADAEVLARKMKGIGTDEDSILNLTARSNAQRQIAEEFKTLFGF 61
 DB 16 ALRGVTFDSGFDGRADAEVLARKMKGIGTDEDSILNLTARSNAQRQIAEEFKTLFGF 75
 QY 62 DLYNDKSELTKGFEKLIYALMKPSRLYDAVELKHAELGAGTDEKVTETIIASRTPEELR 121
 DB 76 DLYNDKSELTKGFEKLIYALMKPSRLYDAVELKHAELGAGTDEKVTETIIASRTPEELR 135
 QY 122 AIKQAYEEYGSNLEDDVVGDTSGYQRMVLVLLQANRDPDTAIDDAQVELDAQALFQAG 181

DB 136 AIKQAYEEYGSNLEDDVVGDTSGYQRMVLVLLQANRDPDTAIDDAQVELDAQALFQAG 195
 QY 182 ELKMGDEEKFITILGTRSVSHLRVYEDKMTISGFOIETTIDRETSQNLLELLAVYK 241
 DB 196 ELKMGDEEKFITILGTRSVSHLRVYEDKMTISGFOIETTIDRETSQNLLELLAVYK 255
 QY 242 IRSIPAYLAETLYYAMKAGTDHTLIRIVSRSEIDLFNIRKPKNFATSLYSMIKG 301
 DB 256 IRSIPAYLAETLYYAMKAGTDHTLIRIVSRSEIDLFNIRKPKNFATSLYSMIKG 315
 QY 302 TSQDYKXALLLCCGEDD 319
 DB 316 TSQDYKXALLLCCGEDD 333

RESULT 3

US-10-007-761-72
 ; Sequence 72, Application US/10007761
 ; Publication No. US20020150984A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Mochly-Rosen, Daria
 ; TITLE OF INVENTION: Peptides for Activation and Inhibition
 ; FILE REFERENCE: 58600-8208-US00
 ; CURRENT APPLICATION NUMBER: US/10/007,761
 ; CURRENT FILING DATE: 2001-11-09
 ; PRIOR APPLICATION NUMBER: US 60/262,060
 ; PRIOR FILING DATE: 2001-01-18
 ; NUMBER OF SEQ ID NOS: 72
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 72
 ; LENGTH: 320
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-007-761-72

Query Match 90.8%; Score 1451.5; DB 14; Length 320;
 Best Local Similarity 91.5%; Pred. No. 2.1e-128;
 Matches 290; Conservative 12; Mismatches 14; Indels 1; Gaps 1;

QY 3 LRGTVDPSGFDGRADAEVLARKMKGIGTDEDSILNLTARSNAQRQIAEEFKTLFGF 62
 DB 5 LRGTVDPSGFDGRADAEVLARKMKGIGTDEDSILNLTARSNAQRQIAEEFKTLFGF 64
 QY 63 LYNDSKSELTKGFEKLIYALMKPSRLYDAVELKHAELGAGTDEKVTETIIASRTPEELR 122
 DB 65 LYNDSKSELTKGFEKLIYALMKPSRLYDAVELKHAELGAGTDEKVTETIIASRTPEELR 124
 QY 123 IKQAYEEYGSNLEDDVVGDTSGYQRMVLVLLQANRDPDTAIDDAQVELDAQALFQAG 182
 DB 125 IKQAYEEYGSNLEDDVVGDTSGYQRMVLVLLQANRDPDTAIDDAQVELDAQALFQAG 184
 QY 183 LKMGDEEKFITILGTRSVSHLRVYEDKMTISGFOIETTIDRETSQNLLELLAVYK 242
 DB 185 LKMGDEEKFITILGTRSVSHLRVYEDKMTISGFOIETTIDRETSQNLLELLAVYK 244
 QY 243 RSIPAYLAETLYYAMKAGTDHTLIRIVSRSEIDLFNIRKPKNFATSLYSMIKG 302
 DB 245 RSIPAYLAETLYYAMKAGTDHTLIRIVSRSEIDLFNIRKPKNFATSLYSMIKG 304
 QY 303 SGDYKXALLLCCGEDD 319
 DB 305 SGDYKXALLLCCGEDD 320

RESULT 4

US-03-970-969-2
 ; Sequence 2, Application US/03970969
 ; Patent No. US20020103341A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Talc, Jonathan F.
 ; APPLICANT: Brown, David S.
 ; TITLE OF INVENTION: Annexin Derivatives with Endogenous Chelation Sites

FILE REFERENCE: ucfw-1-13841
 CURRENT APPLICATION NUMBER: US/09/970,969
 CURRENT FILING DATE: 2001-10-03
 NUMBER OF SEQ ID NOS: 6
 SOFTWARE: Patentn Ver. 2.0
 SEQ ID NO 2
 LENGTH: 327
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-970-969-2

Query Match 90.3%; Score 1442.5; DB 10; Length 327;
 Best Local Similarity 91.2%; Pred. No. 1.6e-127;
 Matches 289; Conservative 12; Mismatches 15; Indels 1; Gaps 1;

QY 3 LRGTVDPSGFGDAEVLKRAMKGLGTDEDSILNLTARSNAQROQIAEFKTLFGSD 62
 DB 12 LRGTVDPSGFGDEADAEVLKRAMKGLGTDEDSILNLTARSNAQROQISAFKTLFGSD 71
 QY 63 LVNDKSELTGKFEKLIYALMKPSRLYDAYELKAKLGAAGTDEKVTETIISRTPEELRA 122
 DB 72 LLDLKSRLTGKFEKLIYALMKPSRLYDAYELKAKLGAAGTDEKVTETIISRTPEELRA 131
 QY 123 IKQAYEEYGSNLEDVVDGTSGYQRMVLVLLQANRPDPAIDDAQVELDAQALFQAGE 182
 DB 132 IKQAYEEYGSNLEDVVDGTSGYQRMVLVLLQANRPDPAIDDAQVELDAQALFQAGE 191
 QY 183 LKMGTDDEKFTITLIGTSVSHLRVDPKMTISGFQIETIDRETSNLEMLLAVKSI 242
 DB 192 LKMGTDDEKFTITLIGTSVSHLRVDPKMTISGFQIETIDRETSNLEMLLAVKSI 251
 QY 243 RSIPIAYLAETLYYAMKAGTDHDLIRVVSSEIDLFINRKEFRKNPATSLYSMIKGD 302
 DB 252 RSIPIAYLAETLYYAMKAGTDHDLIRVVSSEIDLFINRKEFRKNPATSLYSMIKGD 311
 QY 303 SGDYKALLLLCGEED 319
 DB 312 SGDYKALLLL-SEED 327

RESULT 5
 US-09-970-969-4
 Sequence 4, Application US/09970969
 Patent No. US20020103341A1
 GENERAL INFORMATION:
 APPLICANT: Tait, Jonathan F.
 TITLE OF INVENTION: Annexin Derivatives with Endogenous Chelation Sites
 FILE REFERENCE: ucfw-1-13841
 CURRENT APPLICATION NUMBER: US/09/970,969
 CURRENT FILING DATE: 2001-10-03
 NUMBER OF SEQ ID NOS: 6
 SOFTWARE: Patentn Ver. 2.0
 SEQ ID NO 4
 LENGTH: 327
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-970-969-4

Query Match 90.3%; Score 1442.5; DB 10; Length 327;
 Best Local Similarity 91.2%; Pred. No. 1.6e-127;
 Matches 289; Conservative 12; Mismatches 15; Indels 1; Gaps 1;

QY 3 LRGTVDPSGFGDAEVLKRAMKGLGTDEDSILNLTARSNAQROQIAEFKTLFGSD 62
 DB 12 LRGTVDPSGFGDEADAEVLKRAMKGLGTDEDSILNLTARSNAQROQISAFKTLFGSD 71
 QY 63 LVNDKSELTGKFEKLIYALMKPSRLYDAYELKAKLGAAGTDEKVTETIISRTPEELRA 122
 DB 72 LLDLKSRLTGKFEKLIYALMKPSRLYDAYELKAKLGAAGTDEKVTETIISRTPEELRA 131
 QY 123 IKQAYEEYGSNLEDVVDGTSGYQRMVLVLLQANRPDPAIDDAQVELDAQALFQAGE 182

DB 132 IKQAYEEYGSNLEDVVDGTSGYQRMVLVLLQANRPDPAIDDAQVELDAQALFQAGE 191
 QY 183 LKMGTDDEKFTITLIGTSVSHLRVDPKMTISGFQIETIDRETSNLEMLLAVKSI 242
 DB 192 LKMGTDDEKFTITLIGTSVSHLRVDPKMTISGFQIETIDRETSNLEMLLAVKSI 251
 QY 243 RSIPIAYLAETLYYAMKAGTDHDLIRVVSSEIDLFINRKEFRKNPATSLYSMIKGD 302
 DB 252 RSIPIAYLAETLYYAMKAGTDHDLIRVVSSEIDLFINRKEFRKNPATSLYSMIKGD 311
 QY 303 SGDYKALLLLCGEED 319
 DB 312 SGDYKALLLL-SEED 327

RESULT 6
 US-09-970-969-6
 Sequence 6, Application US/09970969
 Patent No. US20020103341A1
 GENERAL INFORMATION:
 APPLICANT: Tait, Jonathan F.
 TITLE OF INVENTION: Annexin Derivatives with Endogenous Chelation Sites
 FILE REFERENCE: ucfw-1-13841
 CURRENT APPLICATION NUMBER: US/09/970,969
 CURRENT FILING DATE: 2001-10-03
 NUMBER OF SEQ ID NOS: 6
 SOFTWARE: Patentn Ver. 2.0
 SEQ ID NO 6
 LENGTH: 327
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-970-969-6

Query Match 90.3%; Score 1442.5; DB 10; Length 327;
 Best Local Similarity 91.2%; Pred. No. 1.6e-127;
 Matches 289; Conservative 12; Mismatches 15; Indels 1; Gaps 1;

QY 3 LRGTVDPSGFGDAEVLKRAMKGLGTDEDSILNLTARSNAQROQIAEFKTLFGSD 62
 DB 12 LRGTVDPSGFGDEADAEVLKRAMKGLGTDEDSILNLTARSNAQROQISAFKTLFGSD 71
 QY 63 LVNDKSELTGKFEKLIYALMKPSRLYDAYELKAKLGAAGTDEKVTETIISRTPEELRA 122
 DB 72 LLDLKSRLTGKFEKLIYALMKPSRLYDAYELKAKLGAAGTDEKVTETIISRTPEELRA 131
 QY 123 IKQAYEEYGSNLEDVVDGTSGYQRMVLVLLQANRPDPAIDDAQVELDAQALFQAGE 182
 DB 132 IKQAYEEYGSNLEDVVDGTSGYQRMVLVLLQANRPDPAIDDAQVELDAQALFQAGE 191
 QY 183 LKMGTDDEKFTITLIGTSVSHLRVDPKMTISGFQIETIDRETSNLEMLLAVKSI 242
 DB 192 LKMGTDDEKFTITLIGTSVSHLRVDPKMTISGFQIETIDRETSNLEMLLAVKSI 251
 QY 243 RSIPIAYLAETLYYAMKAGTDHDLIRVVSSEIDLFINRKEFRKNPATSLYSMIKGD 302
 DB 252 RSIPIAYLAETLYYAMKAGTDHDLIRVVSSEIDLFINRKEFRKNPATSLYSMIKGD 311
 QY 303 SGDYKALLLLCGEED 319
 DB 312 SGDYKALLLL-SEED 327

RESULT 7
 US-10-097-340-10
 Sequence 10, Application US/10097340
 Patent No. US20030087250A1
 GENERAL INFORMATION:
 APPLICANT: John MONAHAN
 TITLE OF INVENTION: Annexin Derivatives with Endogenous Chelation Sites
 FILE REFERENCE: ucfw-1-13841
 CURRENT APPLICATION NUMBER: US/10/097,340
 CURRENT FILING DATE: 2003-08-25
 NUMBER OF SEQ ID NOS: 10
 SOFTWARE: Patentn Ver. 2.0
 SEQ ID NO 10
 LENGTH: 327
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-097-340-10

QY 3 LRGTVDPSGFGDAEVLKRAMKGLGTDEDSILNLTARSNAQROQIAEFKTLFGSD 62
 DB 12 LRGTVDPSGFGDEADAEVLKRAMKGLGTDEDSILNLTARSNAQROQISAFKTLFGSD 71
 QY 63 LVNDKSELTGKFEKLIYALMKPSRLYDAYELKAKLGAAGTDEKVTETIISRTPEELRA 122
 DB 72 LLDLKSRLTGKFEKLIYALMKPSRLYDAYELKAKLGAAGTDEKVTETIISRTPEELRA 131
 QY 123 IKQAYEEYGSNLEDVVDGTSGYQRMVLVLLQANRPDPAIDDAQVELDAQALFQAGE 182

[illegible]

QY 3 LRGTVTDFSGFDGRADAEVLRKAMKGLGTDEDSILNLLTARSNACRQOIAEEFKTLFGRD 62

[illegible]

Db 8 LRGTVDFFPGDGRADAEVLIRKAMKGLGTDDESIINLTLSRSNAORQIEISAFFKTLFGDRD 67
 QY 63 LVNDMKSGLTGKFEKLIIVALKMPSRLYDAVELKHAKEAGTDEKYLTEIIASRTPEELRA 122
 Db 68 LLDLKLKSELTGKFEKLIIVALKMPSRLYDAVELKHAKEAGTDEKYLTEIIASRTPEELRA 127
 QY 123 IKQAYEEYGSNLEDVVGDTSGYQRMVLVLLQANRDPDTAIDDAQVELDAQALFOAGE 182
 Db 128 IKQAYEEYGSNLEDVVGDTSGYQRMVLVLLQANRDPDTAIDDAQVELDAQALFOAGE 187
 QY 183 LKMGDEEKFITITIGTRSV 201
 Db 188 LKMGDEEKFITITIGTRSV 206

RESULT 10
 US-10-236-031B-18
 ; Sequence 18, Application US/10236031B
 ; Publication No. US20030219760A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gordon, Gavin J.
 ; APPLICANT: Jensen, Roderick V.
 ; APPLICANT: Gullans, Steven R.
 ; APPLICANT: Bueno, Raphael
 ; TITLE OF INVENTION: Diagnostic and Prognostic Tests
 ; FILE REFERENCE: B00801/70265 (JRV/JAV)
 ; CURRENT APPLICATION NUMBER: US/10/236, 031B
 ; CURRENT FILING DATE: 2002-09-05
 ; PRIOR APPLICATION NUMBER: US 60/317,389
 ; PRIOR FILING DATE: 2001-09-05
 ; PRIOR APPLICATION NUMBER: US 60/407,431
 ; PRIOR FILING DATE: 2002-08-30
 ; NUMBER OF SEQ ID NOS: 102
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 18
 ; LENGTH: 327
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-236-031B-18

Query Match 51.5%; Score 822.5; DB 12; Length 327;
 Best Local Similarity 56.9%; Pred. No. 3,9e-69;
 Matches 178; Conservative 44; Mismatches 90; Indels 1; Gaps 1;
 QY 6 TVTDFSGDGRADAEVLIRKAMKGLGTDDESIINLTLSRSNAORQIEISAFFKTLFGDRD 65
 Db 14 TVKSSSHFNPDPAETLYKAMKGIQTEQALIDVLRKSNTRQQAISFKAQFQKDLTE 73
 QY 66 DMKSELTGKFEKLIIVALKMPSRLYDAVELKHAKEAGTDEKYLTEIIASRTPEELRAIKQ 125
 Db 74 TLKSELGKFEKLIIVALKMPSRLYDAVELKHAKEAGTDEKYLTEIIASRTPEELRAIKQ 133
 QY 126 AYEERYGSNLEDVVGDTSGYQRMVLVLLQANRDP-DPAIDDAQVELDAQALFOAGELK 184
 Db 134 AYEEDYGSNLEDVVGDTSGYQRMVLVLLQANRDPVSVFPALADQADLVLAAGKGI 193
 QY 185 WGTDEEKFITITIGTRSVSHLRVFDKXMTISGFIQIETTDRFTSGNLENLLAVKXSTRS 244
 Db 194 RGDDEKFIITILCRSTHLLRVFEERKXANKSIDSKSTHSLSEFAMLVKXCTON 253
 QY 245 IPAYIAETLYAMKAGTDDHTLIRIVSRSEIDLPIKREPKNPATSLYMINIKGDTSG 304
 Db 254 LHSYFAERLYAMKAGTDDHTLIRIVSRSEIDLPIKREPKNPATSLYMINIKGDTSG 313
 QY 305 DYKALLLLCGGE 317
 Db 314 DYKALLLLVGS 326

RESULT 11
 US-10-316-253-262
 ; Sequence 262, Application US/10316253
 ; Publication No. US20030162706A1

; GENERAL INFORMATION:
 ; APPLICANT: The Procter & Gamble Company
 ; APPLICANT: Peters, Kevin
 ; APPLICANT: Thompson, Larry
 ; APPLICANT: Wang, Feng
 ; APPLICANT: Greis, Kenneth
 ; TITLE OF INVENTION: Angiogenesis Modulating Proteins
 ; FILE REFERENCE: 8865M
 ; CURRENT APPLICATION NUMBER: US/10/316, 253
 ; CURRENT FILING DATE: 2002-12-10
 ; PRIOR APPLICATION NUMBER: US 60/355,295
 ; PRIOR FILING DATE: 2002-02-08
 ; NUMBER OF SEQ ID NOS: 308
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 262
 ; LENGTH: 324
 ; TYPE: PRT
 ; ORGANISM: Rattus norvegicus
 ; US-10-316-253-262

Query Match 49.2%; Score 787; DB 12; Length 324;
 Best Local Similarity 48.6%; Pred. No. 8,5e-66;
 Matches 153; Conservative 64; Mismatches 98; Indels 0; Gaps 0;
 QY 4 RGTVDFFSGDGRADAEVLIRKAMKGLGTDDESIINLTLSRSNAORQIEISAFFKTLFGDRD 63
 Db 10 RGTINYPGFNSVDHEAIRKAIKIGTDEKTLINILTERSNARQILVHIGQAYQAL 69
 QY 64 VNDMKSGLTGKFEKLIIVALKMPSRLYDAVELKHAKEAGTDEKYLTEIIASRTPEELRAI 123
 Db 70 KADLKDLISGFHEHVMVALITAPAFDAKQKKSRGWTDEDTLIELTFRISROKKEI 129
 QY 124 KQAYEEYGSNLEDVVGDTSGYQRMVLVLLQANRDPDTAIDDAQVELDAQALFOAGEL 183
 Db 130 SQAYTYAYKMLRDISSTSDPFKALTLADGGRDGLKVDEHLAKKQATLYDAGEK 189
 QY 184 KMGDEEKFITITIGTRSVSHLRVFDKXMTISGFIQIETTDRFTSGNLENLLAVKXSTRS 243
 Db 190 KMGDEEKFITITILCRSTHLLRVFEERKXANKSIDSKSTHSLSEFAMLVKXCTON 249
 QY 244 SIPAYIAETLYAMKAGTDDHTLIRIVSRSEIDLPIKREPKNPATSLYMINIKGDTSG 303
 Db 250 NTPAFAGRLHQAAGTDETLNIRIVSRSEIDLPIKREPKNPATSLYMINIKGDTSG 309
 QY 304 GDYKALLLLCGGED 318
 Db 310 GDYRTVLLKICGDD 324

RESULT 12
 US-10-205-823-34
 ; Sequence 34, Application US/10205823
 ; Publication No. US20030108963A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Schlegel, Robert
 ; APPLICANT: Monahan, John B.
 ; APPLICANT: Endege, Wilson O.
 ; APPLICANT: Gannavakapu, Manjula
 ; APPLICANT: Gorbacheva, Bella
 ; APPLICANT: Hoersch, Sebastian
 ; APPLICANT: Kamatkar, Shubhangi
 ; APPLICANT: Monsey, Angela M.
 ; APPLICANT: Glatt, Karen
 ; APPLICANT: Zhao, Xumei
 ; APPLICANT: Anderson, Dustin
 ; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
 ; METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
 ; THERAPY OF PROSTATE CANCER
 ; FILE REFERENCE: MRI-044
 ; CURRENT APPLICATION NUMBER: US/10/205, 823
 ; CURRENT FILING DATE: 2002-07-25
 ; PRIOR APPLICATION NUMBER: 60/307,982
 ; PRIOR FILING DATE: 2001-07-25

Db	173	CGTTRAAAFDAIRDAEILIRKAMKCGTGDGATIDVVAANSNDRCQITKAFSTYSXKDL	232
Oy	64	VNDMSKELTGKEEKELIVALMMPSRLYDYAEIKHAKLGAGTDEKYLTTIISRPEELRAI	123
Db	233	IKDLKEELSGNNEEILILLFEMPTYYDAMSIRKMGAGQGERLIEILOTRNOEIREI	292
Oy	124	KQAESEESYNSNEDDVGDPTSGYQRMVLVLLQANRPDPAIDQAQVELDAQALFOAGEI	183
Db	293	VRYQSEFPRDLKDOI RSDTSGHFERRLLVSMQCQNRBNQNSINQWAGDAQLYQAGSG	352
Oy	184	KMGTDSEKTTILIGTRSVSHLRVVDKMTTSGQIEETIDRETSGLNELLAAVKSIR	243
Db	353	RLQTDSECCNMILATRSFPQLATWAEVSRMANBDLLSVSREBSGYVESGLTTIQCAL	412
Oy	244	SIRAVYAETLLYYAMKGAGTGDHETLIRVVSRSSEIDLFNIRKEPKNATSLYSMIKQDS	303
Db	413	NRAFAFEAEELYYAMKGAGTGDSTLVRIIVTSSSEIDLVIQMFQWQYKTLGTMINGDS	472
Oy	304	GDYKXALLILCG 315	
Db	473	GDYRRLLLAIVG 484	

RESULT 14	US-09-974-298-91
Sequence 91:	Application US/09974298
Patent No.	US20020156263A1
GENERAL INFORMATION:	
APPLICANT:	Chen, Huei-Mei
TITLE OF INVENTION:	GENES EXPRESSED IN BREAST CANCER
FILE REFERENCE:	PA-0037 P
CURRENT APPLICATION NUMBER:	US/09/974,298
CURRENT FILING DATE:	2001-10-04
PRIOR APPLICATION NUMBER:	60/238,331
PRIOR FILING DATE:	2000-05-10
NUMBER OF SEQ. ID NOS:	194
SOFTWARE:	PERL Program
SEQ. ID NO 91	
LENGTH:	339
TYPE:	PRT
ORGANISM:	Homo sapiens
FEATURE:	
NAME/KEY:	misc feature
OTHER INFORMATION:	Incyte ID No. US20020156263A1 1378745CD1
US-09-974-298-91	

Query Match	43.5%; Score 695.5; DB 10; Length 339;
Best Local Similarity	45.4%; Pred. No. 3.7e-57;
Matches 143; Conservative 67; Mismatches 104; Indels 1; Gaps 1	

Oy	5	GTVTDFSGDGRADAEVLRKAMKGLGTDEDSILNLLTARSVAORQCIABEFKTLFGRDLV	64
Db	25	GSVYKATINFDABRDALNITAKTKGVDEVTIVILNRSNAQCQDIAPAYQRTKXELA	84
Oy	65	NDVKSSELTKFEKELIVALKPBRLYDAVELKAKLGAGTDEKYLTEIIASRTDEELPAIK	124
Db	85	SALKSALSHLEITVLIGLTKTPAQYDASELKASKMGKGTDEDSILIEICRTNOEIQEIN	144
Oy	125	QAEVEESYNSNEDDVGDPTSGYQRMVLVLLQANRPDPAIDQAQVELDAQALFOAGEL	183
Db	145	KVYKEMKTKDLEDIISTDSGDFRKLALMAKGRABDGSITVELIDQDARLDYDAGVK	204
Oy	184	KMGTDSEKTTILIGTRSVSHLRVVDKMTTSGQIEETIDRETSGLNELLAAVKSIR	243
Db	205	RKSTDPVKMISINTERSVPHLOKVFDRKYSYSPYDMLESIXEKYKGLLENAFNLVQCIO	264
Oy	244	SIRAVYAETLLYYAMKGAGTGDHETLIRVVSRSSEIDLFNIRKEPKNATSLYSMIKQDS	303
Db	265	NKRLYAPADLLYSMKGKGRDKYLIRINVSSEYDMLKINSEFRKTKGSLYYIYIQDTR	324
Oy	304	GDYKXALLILCGED 318	

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compen Ltd.

OM protein - protein search, using sw model

Run on: December 12, 2003, 14:47:48 ; Search time 10.6549 Seconds
(without alignments)
2879.232 Million cell updates/sec

Title: PCT-US03-24332-3

Perfect score: 1598
Sequence: 1 MALRGVTVPFSGFDGRADAE.....GDTSGDYKALLLCGGEDD 319

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 segs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: PIR_76: *
2: PIR: *
3: PIR: *
4: PIR: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	1585	99.2	1 LURTS	annexin V - rat
2	1467	91.8	320 1 S27214	annexin V - bovine
3	1451.5	90.8	320 1 AQHUP	annexin V [validat
4	1257	78.7	321 1 LUCHS	annexin V - chick
5	934	58.4	673 1 S52844	annexin VI - rat
6	933	58.4	673 1 S01786	annexin VI - mouse
7	921	57.6	321 1 A42077	annexin IV - human
8	919	57.5	673 1 AQH068	annexin VI [valida
9	916	57.3	319 1 LUBO4	annexin IV - bovin
10	915	57.3	318 1 LUP64	annexin IV - pig
11	898	56.2	671 2 JC2029	annexin - chicken
12	876	54.8	503 1 LURB11	annexin XI - rabbi
13	870	54.4	503 1 LUBO11	annexin XI form A
14	870	54.4	505 1 S23447	annexin XI form B
15	858	53.7	505 2 A53152	annexin XI - human
16	822.5	51.5	327 1 LURH8	annexin VIII - hum
17	792	49.6	324 1 LURH3	annexin III - rat
18	785	49.1	323 1 LURH3	annexin III - huma
19	763	47.7	463 2 S29170	annexin VII - mous
20	760	47.6	468 1 LURH7	annexin VII, long
21	718	44.9	316 1 LURF12	annexin XII - Hydr
22	695.5	43.5	339 1 LURH36	annexin II - human
23	695.5	43.5	339 2 S33700	annexin II - rat
24	692	43.3	676 2 S41022	hypothetical prote
25	691.5	43.3	339 1 LUBO36	annexin II - bovin
26	688.5	43.1	339 1 LUM836	annexin II - mouse
27	688.5	42.8	341 2 S55277	annexin II - rat
28	683.5	42.8	340 1 UQ1298	annexin II type 2
29	682.5	42.7	340 1 UQ1297	annexin II type 1

30	680.5	42.6	339 1 LUCH2	annexin II - chick
31	676	42.3	512 2 S70644	annexin VII - Afr
32	675	42.2	296 1 LURF9	annexin IX - fruit
33	673	42.1	316 1 LURH5	annexin XIII, inte
34	671	42.0	321 1 LURF10	annexin X - fruit
35	665	41.6	316 2 A57076	annexin XIIIa - do
36	665	41.6	357 2 B57076	annexin XIIIb - do
37	652	40.8	346 1 LUGP1	annexin I - guinea
38	626	39.2	346 1 S28228	annexin I - bovine
39	622	38.9	346 1 LURH	annexin I - human
40	620	38.8	343 1 A4118	annexin I type 2 -
41	615	38.5	346 1 LURH1	annexin I - rat
42	613	38.4	345 1 LUMS1	annexin I - mouse
43	596.5	37.3	322 2 B8452	protein ZC15.1 [i
44	570.5	35.7	341 1 LURP1	annexin I type 1 -
45	534.5	33.4	462 1 LUD07	annexin VII - sim

ALIGNMENTS

RESULT 1

LURTS

annexin V - rat

N;Alternate names: endonexin II; lipocortin V; placental anticoagulant protein; place

C;Species: Rattus norvegicus (Norway rat)

C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 22-Jun-1999

C;Accession: C29250; S66680

R;Pepinsky, R.B.; Rizard, R.; Mettaliano, R.J.; Sinclair, L.K.; Miller, G.T.; Brownin

J. Biol. Chem. 263, 10799-10811, 1988

A;Title: Five distinct calcium and phospholipid binding proteins share homology with

A;Reference number: A92659; MUID:188273202; PMID:2968983

A;Accession: C29250

A;Molecule type: mRNA

A;Residues: 1-319 <EP>

A;Cross-references: GB:M21730; NID:9205138; PID:AAA4512.1; PID:G205139

R;Imai, Y.; Kohseka, S.

Eur. J. Biochem. 235, 327-334, 1995

A;Title: Structure of rat annexin V gene and molecular diversity of its transcripts.

A;Reference number: S66680; MUID:96035863; PMID:7556178

A;Accession: S66680

A;Status: preliminary; translation not shown

A;Molecule type: DNA

A;Residues: 1-319 <IMA>

A;Cross-references: EMBL:D42136

C;Comment: Annexins undergo reversible, calcium-dependent binding to membrane phospho

deroloid. Annexin V has been proposed to play a role in the inhibition of blood coag

ulation-binding rather than proteolytic inactivation. It does not affect thrombin-depe

C;Genetics: 1/3; 30/1; 61/3; 99/3; 130/1; 156/3; 175/3; 207/1; 239/1; 258/3; 299/3

C;Superfamily: annexin I; annexin repeat homology

C;Keywords: calcium binding; duplication; endonexin fold; membrane-associated protein

F;2-319/Product: annexin V #status predicted <MNT>

F;16-87/Domains: annexin repeat homology <AX1>

F;27-43/Region: endonexin fold #status predicted

F;88-159/Domains: annexin repeat homology <AX2>

F;99-115/Region: endonexin fold #status predicted

F;171-243/Domains: annexin repeat homology <AX3>

F;183-199/Region: endonexin fold #status predicted

F;247-318/Domains: annexin repeat homology <AX4>

F;258-274/Region: endonexin fold #status predicted

F;26-28-30-70/Binding site: calcium, high affinity (Met, Gly, Glu) #status predi

F;31-33-34/Binding site: calcium, low affinity (Thr, Glu, Asp) #status predicted

F;71-76/Binding site: calcium, low affinity (Leu, Glu) #status predicted

F;98-100-102-142/Binding site: calcium, high affinity (Leu, Gly, Asp) #status pr

F;257-259-261-301/Binding site: calcium, high affinity (Met, Gly, Asp) #status F

Query Match 99.2% Score 1585; DB 1; Length 319;

Best Local Similarity 99.4% Pred. No. 5.1e-96;

Matches 317; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MALRGVTVPFSGFDGRADAEVLRKAKKGLGTDDEDSINLTLFARNAPQQAIEEFKILFG 60

```

Db      1 MALRTVTDPSGFGDRAAEVLRKMKLGTDDESIINLITANSNQRQOIAEFTTLFG 60
QY      61 RDLVNDMKSSELTGKEFKIIVALKMPSRLYDAVELKAKLGAAGDEKVLTEIIASRPEEL 120
Db      61 RDLVNDMKSSELTGKEFKIIVALKMPSRLYDAVELKAKLGAAGDEKVLTEIIASRPEEL 120
QY      121 RAIKQAYEEYGSNNLEDDVVGDTSGYGRMLVLLQANRPDPAIDDAQVELDAQALFQAGE 180
Db      121 RAIKQAYEEYGSNNLEDDVVGDTSGYGRMLVLLQANRPDPAIDDAQVELDAQALFQAGE 180
QY      181 GELKMGTDDEKFTITLIGRSVSHLRVFDKMTTISGFQIETITDRETSGNLEMLLAVVK 240
Db      181 GELKMGTDDEKFTITLIGRSVSHLRVFDKMTTISGFQIETITDRETSGNLEMLLAVVK 240
QY      241 SIRSIPAYLAETLYYAMKAGAGTDHTLLRVVSSSEIDLVRIRKFRKNATSLYSMKG 300
Db      241 SIRSIPAYLAETLYYAMKAGAGTDHTLLRVVSSSEIDLVRIRKFRKNATSLYSMKG 300
QY      301 DTSGDYKALLLLCGGEDD 319
Db      301 DTSGDYKALLLLCGGEDD 319

```

RESULT 2

```

S27214
Name: annexin V - bovine
N/Alternate names: CaBP3; CaBP37
C/Species: Bos primigenius taurus (cattle)
C/Date: 08-Jun-1994 #sequence_revision 10-Feb-1995 #text_change 26-Feb-1999
C/Accession: S27214; S27215
R/Location: M.P.; Howell, S.A.; Harris, A.C.M.; Ames, B.; Patel, Y.; Giambanco, I.; Bi
Biochem. Biophys. Acta 1160, 76-83, 1992
A/Title: Novel isoforms of CaBP 33/37 (Annexin V) from mammalian brain: structural and f
A/Reference number: S27214; MUID:93041974; PMID:1420335
A/Accession: S27214
A/Molecule type: protein
A/Residues: 1-320 <LEA>
A/Accession: S27215
A/Molecule type: protein
A/Residues: 1-35; 'T', 37-124, 'E', 126-320 <LE2>
A/Note: It is uncertain whether the sequence differences are due to allelic variation or
C/Comment: Annexins undergo reversible, calcium-dependent binding to membrane phospholip
C/Comment: Annexin V has been proposed to play a role in the inhibition of blood coagula
Oligo-binding rather than proteolytic inactivation. It does not affect thrombin-depende
C/Superfamily: annexin I; annexin repeat homology
C/Keywords: acetylated amino end; anticoagulant; calcium binding; duplication; endonexin
F/17-88/Domain: annexin repeat homology <AX1>
F/28-44/Region: endonexin fold #status predicted
F/89-160/Domain: annexin repeat homology <AX2>
F/100-116/Region: endonexin fold #status predicted
F/172-244/Domain: annexin repeat homology <AX3>
F/184-200/Region: endonexin fold #status predicted
F/248-319/Domain: annexin repeat homology <AX4>
F/259-275/Region: endonexin fold #status predicted
F/1/Modified site: acetylated amino end (Ala) #status experimental
F/22/Binding site: phosphate (Thr) (covalent) #status experimental
F/27-29-31-71/Binding site: calcium, high affinity (Thr, Gly, Gly, Glu) #status predicte
F/32-34-35/Binding site: calcium, low affinity (Thr, Gly, Glu) #status predicted
F/72-77/Binding site: calcium, low affinity (Leu, Glu) #status predicted
F/99-101-103-143/Binding site: calcium, high affinity (Leu, Gly, Gly, Asp) #status predi
F/258-260-262-302/Binding site: calcium, high affinity (Met, Gly, Gly, Asp) #status pred

```

Query Match 91.8%; Score 1467; DB 1; Length 320;

Best local similarity 91.8%; Pred. No. 2-4e-89;

Matches 291; Conservative 10; Mismatches 16; Indels 0; Gaps 0;

```

QY      3 LRGTVTDESGFGDRAAEVLRKMKLGTDDESIINLITANSNQRQOIAEFTTLFG 62
Db      4 LRGTVADPFGFPERADAETLRKMKLGTDDESIITLITRSNQRQOIAEFTTLFG 63
QY      63 LVNDMKSSELTGKEFKIIVALKMPSRLYDAVELKAKLGAAGDEKVLTEIIASRPEELRA 122

```

```

Db      64 LDDLSSELTGKEFKIIVALKMPSRLYDAVELKAKLGAAGDEKVLTEIIASRPEELRA 123
QY      123 IKQAYEEYGSNNLEDDVVGDTSGYGRMLVLLQANRPDPAIDDAQVELDAQALFQAGE 182
Db      124 IKQAYEEYGSNNLEDDVVGDTSGYGRMLVLLQANRPDPAIDDAQVELDAQALFQAGE 183
QY      183 LKMGTDDEKFTITLIGRSVSHLRVFDKMTTISGFQIETITDRETSGNLEMLLAVKSI 242
Db      184 LKMGTDDEKFTITLIGRSVSHLRVFDKMTTISGFQIETITDRETSGNLEMLLAVKSI 243
QY      243 RSIPAYLAETLYYAMKAGAGTDHTLLRVVSSSEIDLVRIRKFRKNATSLYSMKG 302
Db      244 RSIPAYLAETLYYAMKAGAGTDHTLLRVVSSSEIDLVRIRKFRKNATSLYSMKG 303
QY      303 SGDYKALLLLCGGEDD 319
Db      304 SGDYKALLLLCGGEDD 320

```

RESULT 3

ACHUP

annexin V (validated) - human

N/Alternate names: endonexin II; lipocortin V; placental anticoagulant protein; plac

C/Species: Homo sapiens (man)

C/Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 08-Dec-2000

C/Accession: D29250; A30206; A28076; S01016; A29417; A41514; A28038; C31953; S0646;

R/Peptidase, R.B.; Tizabi, R.; Matcaliano, R.J.; Sincclair, L.K.; Miller, G.T.; Brown

J. Biol. Chem. 263, 10759-10811, 1988

A/Title: Five distinct calcium and phospholipid binding proteins share homology with

A/Reference number: A28559; MUID:88273202; PMID:2868983

A/Accession: D29250

A/Molecule type: mRNA

A/Residues: 1-320 <PPP>

A/Cross-references: GB:017131; NID:G186569; PIDN:AAA6166.1; PID:G307116

R/Grundmann, U.; Abel, K.J.; Bohm, H.; Loebmann, H.; Lottepeich, F.; Kuepper, H.

Proc. Natl. Acad. Sci. U.S.A. 85, 3708-3712, 1988

A/Title: Characterization of cDNA encoding human placental anticoagulant protein (Pp

A/Reference number: A30206; MUID:88234495; PMID:2867495

A/Accession: A30206

A/Molecule type: mRNA

A/Residues: 1-320 <GRU>

A/Cross-references: GB:M19384; NID:G189614; PIDN:AA55545.1; PID:G189615

R/Kaplan, R.; Dave, M.; Burgess, W.H.; Schlaepfer, D.D.; Haigler, H.T.

J. Biol. Chem. 263, 8037-8043, 1988

A/Title: Cloning and expression of cDNA for human endonexin II, a Ca(2+) and phospho

A/Reference number: A28076; MUID:88228020; PMID:2867291

A/Accession: A28076

A/Molecule type: mRNA

A/Residues: 1-320 <KAP>

A/Cross-references: GB:003745; NID:G182111; PIDN:AA52386.1; PID:G182112

R/Mauner-Fogel, I.; Reutlinger-Sperger, C.P.M.; Plesters, J.; Bodo, G.; Strassowa, C.; Ha

Eur. J. Biochem. 174, 585-592, 1988

A/Title: Cloning and expression of cDNA for human vascular anticoagulant, a Ca-depen

A/Reference number: S01016; MUID:88271329; PMID:2455636

A/Accession: S01016

A/Molecule type: mRNA

A/Residues: 1-320 <MAV>

A/Cross-references: EMBL:X12454; NID:G37636; PIDN:CAA30985.1; PID:G37637

A/Note: part of this sequence was confirmed by protein sequencing

R/Funkkoht, I.; Hendrickson, L.E.; McMullen, B.A.; Fujikawa, K.

Biochemistry 26, 8087-8092, 1987

A/Title: Primary structure of human placental anticoagulant protein.

A/Reference number: A29417; MUID:88163463; PMID:2864863

A/Contents: amino-terminal acetylation

A/Accession: A29417

A/Molecule type: RNA

A/Residues: 1-320 <FUN>

A/Cross-references: EMBL:M18366; NID:G179131; PIDN:AAA3570.1; PID:G179132

R/Riwaaki, A.; Suda, M.; Nakao, H.; Nagoya, T.; Saito, Y.; Arai, K.; Wazuguchi, T.;

J. Biochem. 102, 1261-1273, 1987

A/Title: Structure and expression of cDNA for an inhibitor of blood coagulation iscl

A/Reference number: A41514; MUID:88192278; PMID:2963810

F:73,78/Binding site: calcium, low affinity (Ieu, Glu) #status experimental
F:100,102,104,144/Binding site: calcium, high affinity (Ieu, Gly, Gly, Asp) #status experimental
F:259,261,263,303/Binding site: calcium, high affinity (Met, Gly, Gly, Asp) #status experimental

Query Match 90.8%; Score 1451.5; DB 1; Length 320;
Best Local Similarity 91.5%; Pred. No. 2,5e-87;
Matches 290; Conservative 12; Mismatches 14; Indels 1; Gaps 1;

Query 3 LRGVVDFSGFDGRADAENVLRKMKGLGDEDSILNLTTPRSNAQOQIAEKKTLFGPD 62
Db LRGVIVDFPSPDERRADETLRKMKGLGDEBSILTLTSRSNAQOQIEISAATKTLFGPD 64
Query 63 LVNDMKSELGKKEKTLVALMKPSRLYDAVELKHALGAGDKEKVTETIIASRPEELRA 122
Db LDDDKSELGKREKTLVALMKPSRLYDAVELKHALKGAGTKENVLTETIASRPEELRA 124
Query 123 IKQAVIEEYFSNLEDVVGSTSGYQRMVLVLQANRPDPTALDDAQVELDAQALPAGE 182
Db IKQVIEEYSSSLEDVVGSTSGYQRMVLVLQANRPDPAGIDAEQVBDQAALPAGE 184
Query 183 LKMGTDPEKRTTLTGTRSVSHLRVFPDKWMTISGFOIEETIDRETSGNLENTLLAVKSI 242
Db LKMGTDPEKRTTLTGTRSVSHLRVFPDKWMTISGFOIEETIDRETSGNLENTLLAVKSI 244
Query 243 RSLPVAIAETLYYAMKAGAGTDHLLIRVIVSRSEIDLFNIRKEFRKNPATSLYSMTKGT 302
Db RSLPVAIAETLYYAMKAGAGTDHLLIRVIVSRSEIDLFNIRKEFRKNPATSLYSMTKGT 304
Query 303 SGDYKKALLLGGEDD 319
Db SGDYKKALLLGGEDD 320

RESULT 4
LUNGS
annexin V - chicken
N/Alternate names: annexin CTI; endonexin II; lipocortin V; placental anticoagulant p
C/Species: Gallus gallus (chicken).
C/Date: 30-Sep-1992 #sequence, revision 30-Sep-1992 #ext_change 02-Jun-2000
C/Accession: A35381; A28623; B40404; S32523; S08771
R/Fernandez, M.P.; Selman, O.; Martin, G.R.; Yamada, Y.; Pfaeffle, M.; Deutzmann, R.;
J. Biol. Chem. 265, 8344, 1990
A/Reference number: A35381; MUID:90243721; PMID:2159478
A/Contents: extralum
A/Accession: A35381
A/Molecule type: mRNA
A/Residues: 1-321 <FEPR>
A/Cross-references: GB:J030971; GB:J03194; NID:G211138; PIDN:AAA48591.1; PID:G211139
R/Fernandez, M.P.; Selman, O.; Martin, G.R.; Yamada, Y.; Pfaeffle, M.; Deutzmann, R.;
J. Biol. Chem. 263, 5921-5925, 1988
A/Title: The structure of annexin CTI, a collagen binding protein isolated from chon
A/Reference number: A28623; MUID:8186917; PMID:2833522
A/Accession: A28623
A/Molecule type: mRNA
A/Residues: 1-118; 'LBKCRILRFNMQEYANLGNKRTIGRSHQAFRDCCWMSCCRQIEI',163-167,'E',169-324
A/Cross-references: GB:M30971; GB:J03194; NID:G211138
R/Genge, B.R.; Wu, L.N.Y.; Adkisson IV, H.D.; Wuthier, R.E.
J. Biol. Chem. 266, 10678-10685, 1991
A/Title: Matrix vesicle annexins exhibit proteolipid-like properties. Selective parti
A/Reference number: A40404; MUID:91244852; PMID:2037607
A/Accession: B40404
A/Molecule type: protein
A/Residues: 168-199 <GEN>
A/Experimental source: epiphyseal growth plate cartilage (matrix vesicle-enriched mid
R/Boustead, C.M.; Brown, R.; Walker, J.H.
Biochem. J. 291, 601-608, 1993
A/Title: Isolation, characterization and localization of annexin V from chicken livern
A/Reference number: S32523; MUID:93249384; PMID:8484740
A/Accession: S32523
A/Status: preliminary
A/Molecule type: protein
A/Residues: 6-20,85,'X',87-88,'X',90-93,'X',95-96,'XX',99-100,'X',102-103,'XX',106-10
C/Comment: Annexins undergo reversible, calcium-dependent binding to membrane phospho

denoted.
 C/Comment: Annexin V has been proposed to play a role in the inhibition of blood coagula-
 Clapd-binding rather than proteolytic inactivation. It does not affect thrombin-depende
 C/Superfamily: annexin I; annexin repeat homology
 C/Keywords: calcium binding; collagen binding; duplication; endonexin fold; membrane-ass
 F/2-31/Region: annexin repeat homology <AX1>
 F/18-89/Domain: annexin repeat homology <AX1>
 F/29-45/Region: endonexin fold #status predicted
 F/101-161/Domain: annexin repeat homology <AX2>
 F/101-117/Region: endonexin fold #status predicted
 F/1173-245/Domain: annexin repeat homology <AX3>
 F/1185-201/Region: endonexin fold #status predicted
 F/1249-320/Domain: annexin repeat homology <AX4>
 F/260-276/Region: endonexin fold #status predicted
 F/28-30/32/72/Binding site: calcium, high affinity (Met, Gly, Gly, Glu) #status predicted
 F/33-35/36/Binding site: calcium, low affinity (Thr, Glu, Glu) #status predicted
 F/73-78/Binding site: calcium, low affinity (Leu, Glu, Glu) #status predicted
 F/100-102,104,144/Binding site: calcium, high affinity (Ile, Gly, Gly, Glu) #status pred
 F/259,261,263,303/Binding site: calcium, high affinity (Met, Gly, Asp) #status pred

Query Match

78.7%; Score 1257; DB 1; Length 321;
 Best Local Similarity 77.2%; Pred. No. 11e-74;

Matches 244; Conservative 39; Mismatches 33; Indels 0; Gaps 0;

QY 4 RGVYTFSGDGRADAEVLRKMGKIGTDEDSILNLTARSNAQROQIAEEFKTLFGRL 63
 Db 6 RGVYAFSPFPARADAEVLRKMGKIGTDEETIKLITSHNNAQROEIASAFKTLFGRL 65
 QY 64 VNDKSELTKFEKLIYALMKESRLVDAELKHAUKAGCTDEVLEITIASRPEELRAI 123
 Db 66 VDDKSELTKFEKLIYALMKESRLVDAELKHAUKAGCTDEVLEITIASRPEELRAI 125
 QY 124 KQAYEEYGSNLEDVVGDTSGYQRMVLLQANRDPDAIDDAQVELDAQALFOAGEL 183
 Db 126 KQVWQYEAHLNLEKDTIGETSGHQLVLLQANRDPDGRVDEALVEXDAQVLPFAGEL 185
 QY 184 KMGTDDEKFTITLIGTSVSHLRVFDKXMTISGQIEETIDRETSGLNENLLAVVKSIR 243
 Db 186 KMGTDDEKFTITLIGTSVSHLRVFDKXMTISGQIEETIDRETSGLNENLLAVVKSIR 245
 QY 244 SIPAYLAETLYAMKAGCTDDHTLIRIVSRSEIDLFINIRKFRKPFATISYMTKGDTS 303
 Db 246 SVPAYFAETLYAMKAGCTDDHTLIRIVSRSEIDLFINIRKFRKPFATISYMTKGDTS 305
 QY 304 GDYKALLLLCGGEDD 319
 Db 306 GDYKALLLLCGGEDD 321

RESULT 5

S52844
 N/Alternate names: calcium-binding protein 65/67
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C/Accession: S65683; S52844
 R/Moss, S.E.; Crumpton, M.R.; Reutter, W.
 Eur. J. Biochem. 230, 741-751, 1995
 A/Title: cDNA cloning and tissue-specific regulation of expression of rat calcium-bindin
 A/Reference number: S65683; MUID:9531313; PMID:7607247
 A/Accession: S65683
 A/Molecule type: mRNA
 A/Residues: 1-673 <MAN>
 A/Cross-references: EMBL:X86086; NID:G763180; PIDN:CAM60040.1; PID:G763181
 A/Experimental source: liver
 C/Superfamily: annexin VI; annexin repeat homology
 C/Keywords: acetylated amino end; calcium binding; endonexin fold; membrane-associated
 F/2-673/Region: annexin VI #status predicted <MAN>
 F/23-94/Domain: annexin repeat homology <AX1>
 F/134-50/Region: endonexin fold #status predicted
 F/195-166/Domain: annexin repeat homology <AX2>
 F/106-122/Region: endonexin fold #status predicted
 F/178-250/Domain: annexin repeat homology <AX3>

F/199-206/Region: endonexin fold #status predicted
 F/254-325/Domain: annexin repeat homology <AX4>
 F/265-281/Region: endonexin fold #status predicted
 F/366-437/Domain: annexin repeat homology <AX5>
 F/377-393/Region: endonexin fold #status predicted
 F/438-509/Domain: annexin repeat homology <AX6>
 F/448-465/Region: endonexin fold #status predicted
 F/527-598/Domain: annexin repeat homology <AX7>
 F/536-554/Region: endonexin fold #status predicted
 F/602-673/Domain: annexin repeat homology <AX8>
 F/613-629/Region: endonexin fold #status predicted
 F/2/Modified site: acetylated amino end (Ala) (in mature form) #status predicted

Query Match

58.4%; Score 934; DB 1; Length 673;
 Best Local Similarity 57.9%; Pred. No. 2.9e-53;

Matches 183; Conservative 54; Mismatches 79; Indels 0; Gaps 0;

QY 4 RGVYTFSGDGRADAEVLRKMGKIGTDEDSILNLTARSNAQROQIAEEFKTLFGRL 63
 Db 11 RGVYDFADPDANQDAEALYTMKFGSDKSEILTLIRSNKQROEIQGYSKLYGRL 70
 QY 64 VNDKSELTKFEKLIYALMKESRLVDAELKHAUKAGCTDEVLEITIASRPEELRAI 123
 Db 71 IADKTELTKFEKLIYALMKESRLVDAELKHAUKAGCTDEVLEITIASRPEELRAI 130
 QY 124 KQAYEEYGSNLEDVVGDTSGYQRMVLLQANRDPDAIDDAQVELDAQALFOAGEL 183
 Db 131 VAAYKQAYERDLESDILGDTSGHQLVLLQANRDPDGRVDEALVEXDAQVLPFAGEL 190
 QY 184 KMGTDDEKFTITLIGTSVSHLRVFDKXMTISGQIEETIDRETSGLNENLLAVVKSIR 243
 Db 191 KMGTDDEKFTITLIGTSVSHLRVFDKXMTISGQIEETIDRETSGLNENLLAVVKSIR 250
 QY 244 SIPAYLAETLYAMKAGCTDDHTLIRIVSRSEIDLFINIRKFRKPFATISYMTKGDTS 303
 Db 251 STEPYFAERLFRKMGKIGTDDHTLIRIVSRSEIDLFINIRKFRKPFATISYMTKGDTS 310
 QY 304 GDYKALLLLCGGEDD 319
 Db 311 GEYKALLLLCGGEDD 326

RESULT 6

S01786
 N/Alternate names: calcium-binding protein p68; calelectrin; calphobindin II
 C/Species: Mus musculus (house mouse)
 C/Date: 30-Sep-1989 #sequence_revision 26-May-1994 #text_change 22-Jun-1999
 C/Accession: S01786
 R/Moss, S.E.; Crumpton, M.R.; Crumpton, M.W.
 Eur. J. Biochem. 177, 21-27, 1988
 A/Title: Molecular cloning of murine p68, a Ca-binding protein of the lipocortin fami
 A/Reference number: S01786; MUID:89030687; PMID:2972541
 A/Accession: S01786
 A/Molecule type: mRNA
 A/Residues: 1-673 <MOS>
 A/Cross-references: EMBL:X13460; NID:953580; PIDN:CAA31808.1; PID:953581
 A/Note: The authors translated the codon GCC for residue 329 as Gly
 C/Comment: This abundant cytosolic protein binds to the inner surface of the cell men
 C/Superfamily: annexin VI; annexin repeat homology
 C/Keywords: acetylated amino end; calcium binding; duplication; endonexin fold; phosph
 F/2-673/Region: annexin VI #status predicted <MAN>
 F/23-94/Domain: annexin repeat homology <AX1>
 F/134-50/Region: endonexin fold #status predicted
 F/195-166/Domain: annexin repeat homology <AX2>
 F/106-122/Region: endonexin fold #status predicted
 F/1106-122/Region: endonexin fold #status predicted
 F/1178-250/Domain: annexin repeat homology <AX3>
 F/1190-206/Region: endonexin fold #status predicted
 F/1254-325/Domain: annexin repeat homology <AX4>
 F/1265-281/Region: endonexin fold #status predicted
 F/1366-437/Domain: annexin repeat homology <AX5>
 F/1377-393/Region: endonexin fold #status predicted
 F/438-509/Domain: annexin repeat homology <AX6>

F:448-465/Region: endonexin fold #status predicted
 F:527-538/Domain: annexin repeat homology <AX7>
 F:538-554/Region: endonexin fold #status predicted
 F:602-673/Domain: annexin repeat homology <AX8>
 F:613-629/Region: endonexin fold #status predicted
 F:2/Modified site: acetylated amino end (Ala) (in mature form) #status predicted

Query Match 58.4%; Score 933; DB 1; Length 673;
 Best Local Similarity 57.8%; Pred. No. 3.3e-53;
 Matches 183; Conservative 53; Mismatches 80; Indels 0; Gaps 0;

QY 4 RGVTFDSGFGDGRADAEVLRKAMKGLGTDSDSTINLLTRSNAPRQQAEEFKTLFGEDL 63
 DB 11 RGSHTDPDFDADQADALATAMKFGSGKESLIELITRSKQKQKQKQKQKQKQKQKQK 70
 QY 64 VNMKSELTKGFEKLVALLMKPSRLVDAYELKAKLGAQTEKVLTEIISTPEELPAI 123
 DB 71 IEDLYELTKGFELIYNLMRPLAYCDAKEIKDAISGIGTDEKCLIEIILASTRNQMRQL 130
 QY 124 KQAYEEYGSNLDDVDVGTSGYQSMVLVLLQANRDPDTAIDDAQVELDAQALFQAGEL 183
 DB 131 VAAVKDAVERKDLESDIIGTSGHFGKMLVLLQGTRENDVDVSEDLVQDDVDLYEAGEL 190
 QY 184 KMGTDSEKFTITIGTSVSHLRVFPKXMTISGFOIEETIDETSGNLEMLLAVKSIK 243
 DB 191 KMGTFDAQFIYILGNRSKQHLRVFDEYELTKTKPIEASIRGELSGDFKMLAVKQICR 250
 QY 244 SIPIYLAETLYAMKAGTDHLLIVISRSIDLFNIRKFRKRFASLYSMKGTGS 303
 DB 251 STEPIFAERLPKAMKGLGTRDNTLIRIMVSRSELDMLDIRIFRTYKESLYSMKNDTS 310
 QY 304 GDYKKALLLGGEDD 319
 DB 311 GEYKKALLKCGGDD 326

RESULT 7

A42077
 annexin IV - human

N/Alternate names: endonexin I, placental anticoagulant protein II, PP4-X protein

C/Species: Homo sapiens (man)

C/Date: 30-Jan-1993 #sequence revision 26-May-1994 #text_change 22-Jun-1999

C/Accession: A42077; B42077; S07434; A11953; A31046

R/Title: J.C., Smith, C.; Frankenberg, D.A.; Mao, C.H.; Adler, D.A.; Distche, C.M.

Genomics 12, 313-318, 1992

A/Title: Chromosomal mapping of the human annexin IV (ANX4) gene.

A/Reference number: A42077; UID:92155721; PMID:1346776

A/Accession: A42077

A/Molecule type: mRNA

A/Residues: 1-321 <TA1>

A/Cross-References: GB:M82809; NID:G178698; PIDN:AA51740.1; PID:G178699

A/Accession: B42077

A/Molecule type: DNA

A/Residues: 87-129 <TA2>

R/Grundmann, U.; Amann, E.; Kuepper, H.A.

Behring Inst. Mitt. 82, 59-67, 1988

A/Title: Isolation and expression of cDNA coding for a new member of the phospholipase A

A/Reference number: S07434; UID:88309022; PMID:2570257

A/Accession: S07434

A/Molecule type: mRNA

A/Residues: 1-97 <Q> 99-321 <GRU>

A/Cross-References: EMBL:M9383; NID:G189616; PIDN:AA041689.1; PID:G189617

R/Ahn, N.G.; Teller, D.C.; Bielekowsky, M.J.; McMullen, B.A.; Lipkin, E.W.; de Haen, C.

J. Biol. Chem. 263, 18657-18663, 1988

A/Title: Sedimentation equilibrium analysis of five lipocortin-related phospholipase A-2

A/Reference number: A92696; UID:89066532; PMID:2974032

A/Accession: A31953

A/Molecule type: protein

A/Residues: 29-58,101-126,282-310 <ARN>

R/Tal, U.F.; Sakata, M.; McMullen, B.A.; Mao, C.H.; Funakoshi, T.; Hendrickson, L.E.;

Biochemistry 27, 6268-6276, 1988

A/Title: Placental anticoagulant proteins: isolation and comparative characterization

A/Reference number: A90534; UID:89118212; PMID:2975506

A/Accession: A31046

A/Molecule type: protein

A/Residues: 4-17,30-74,102-146,283-321 <TA3>

C/Genetics:

A/Genes: GDB:ANX4

A/Cross-References: GDB:131395; OMTM:106491

A/Map position: 2p13-2p13

A/Intons: 102/3

C/Superfamily: annexin I; annexin repeat homology

F:2-321/Product: annexin IV #status predicted <AT>

F:12-90/Domain: annexin repeat homology <AX1>

F:30-46/Region: endonexin fold #status predicted

F:91-162/Domain: annexin repeat homology <AX2>

F:102-118/Region: endonexin fold #status predicted

F:174-246/Domain: annexin repeat homology <AX3>

F:186-202/Region: endonexin fold #status predicted

F:250-321/Domain: annexin repeat homology <AX4>

F:261-277/Region: endonexin fold #status predicted

F:2/Modified site: acetylated amino end (Ala) (in mature form) #status predicted

F:9/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

F:247/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 57.6%; Score 921; DB 1; Length 321;
 Best Local Similarity 57.3%; Pred. No. 8e-53;
 Matches 180; Conservative 56; Mismatches 78; Indels 0; Gaps 0;

QY 5 GIVTFDSGFGDGRADAEVLRKAMKGLGTDSDSTINLLTRSNAPRQQAEEFKTLFGEDL 64
 DB 8 GTVKAASGNAMEDAQTRKAMKGLGTDSDSTINLLTRSNAPRQQAEEFKTLFGEDL 67
 QY 65 NNMKSELTKGFEKLVALLMKPSRLVDAYELKAKLGAQTEKVLTEIISTPEELPAI 124
 DB 68 DDKSELSNPFQVIVGMFTVLYVOELRRANKAGTDGCLIEIILASTPEELPAI 127
 QY 125 QAYEEYGSNLDDVDVGTSGYQSMVLVLLQANRDPDTAIDDAQVELDAQALFQAGEL 184
 DB 128 QTVQQGYSGLDDIRSDTSFVQVILVLSANGRDEENVYDIALVQDDVDLYEAGEL 187
 QY 185 KMGTDSEKFTITIGTSVSHLRVFPKXMTISGFOIEETIDETSGNLEMLLAVKSIK 244
 DB 188 KMGTFDAQFIYILGNRSKQHLRVFDEYELTKTKPIEASIRGELSGDFKMLAVKQICR 247
 QY 244 SIPIYLAETLYAMKAGTDHLLIVISRSIDLFNIRKFRKRFASLYSMKGTGS 304
 DB 248 KSAVFAERLPKAMKGLGTRDNTLIRIMVSRSELDMLDIRIFRTYKESLYSMKNDTS 307
 QY 305 DYKKALLLGGEDD 318
 DB 308 DYRKALLVLCGGDD 321

RESULT 8

AQHU68
 annexin VI [validated] - human

N/Alternate names: calcium-binding protein, 68k, calelectrin, calphobindin II

C/Species: Homo sapiens (man)

C/Date: 31-Mar-1992 #sequence revision 30-Sep-1992 #text_change 08-Dec-2000

C/Accession: J00032; S00263; S18519; A31091; B34459; B31953; A33507

R/Iwasaki, A.; Suda, M.; Watanabe, M.; Nakao, H.; Hattori, Y.; Nagoya, T.; Sano, Y.

J. Biochem. 106, 43-49, 1989

A/Title: Structure and expression of cDNA for calphobindin II, a human placental coag

A/Reference number: J00032; UID:89380132; PMID:2528541

A/Accession: J00032

A/Molecule type: mRNA

A/Residues: 1-675 <IWA>

A/Cross-References: EMBL:J000510; NID:G219550; PIDN:BA00400.1; PID:G219551

R/Crompton, M.R.; Owens, R.J.; Toty, N.F.; Mose, S.E.; Waterfield, M.D.; Crompton, M

EMBO J. 7, 21-27, 1988

A/Title: Primary structure of the human, membrane-associated Ca(2+)-binding protein p

A/Reference number: S00263; UID:89196081; PMID:33258820

F:184-200/Region: endonexin fold #status predicted
 F:248-319/Domain: annexin repeat homology <AX4>
 F:259-275/Region: endonexin fold #status predicted
 F:7/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted
 F:125/245/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 57.3%; Score 916; DB 1; Length 319;
 Best Local Similarity 57.3%; Pred. No. 1.7e-52;
 Matches 180; Conservative 54; Mismatches 80; Indels 0; Gaps 0;

QY 5 GTVTDFSGFDGRADAEVLKRAMKGLTDEDSITLNTLARSNAQROIAEERKTLFGRLV 64
 DB 6 GTVKAASGFMAEDADQLTKRAMKGLTDEDAIINLAVRSTQOEIRAKYKTTIGRLM 65
 QY 65 NDMKSELGKREKLIIVALKMPSRLYDAVELKNAKLGAGDEKVLTEIIASRPEELPAIK 124
 DB 66 DDLKSELGNEQVILGMMPTLVYDQELRRAMKAGDEGCLLEIIASRPEELIRIN 125
 QY 125 QAYEEYGSNLEDVVDGTSGYQRMVLVLLQANRDPDTAIDDAQVELDAQALFOAGELK 184
 DB 126 QTYOQYGRSLIEDDIRSTSPMFQRLVLSAGRDESNVLDALMQDAQDLVEAGEKK 185
 QY 185 WGTDEKFTITLIGRSVSHLRVDPKMTISGFOIEETIDRETSGNLENTLLAVKSI 244
 DB 186 WGTDEVKFLVLCSENRNHLHFDEYKRIAQKDIEQISKTSGSFEDALLAIVKCMRN 245
 QY 245 IPAYLAETLYYAMKAGTDHDLIRVVSSEIDLFNIRKPRKPFATSLYSMTIKGDTSG 304
 DB 246 KSAIFYAEELYSKMGKLTDDTLIRVVSRAEIMDLIRANKRLYKSLYSFIKGDTS 305
 QY 305 DYKXALLILCGED 318
 DB 306 DYKXVLLILCGED 319

RESULT 10

LUP64
 N:Annexin IV - pig
 C/Species: Sus scrofa domestica (domestic pig)
 C/Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 24-Nov-1999
 C/Accession: A27107
 R:Weber, K.; Johanson, N.; Plessmann, U.; Van, P.N.; Soling, H.D.; Ampe, C.; Vandekerckh
 EMBO J. 6: 1599-1604, 1987
 A:Title: The amino acid sequence of protein II and its phosphorylation site for protein
 A:Reference number: A27107; MUID:87275850; PMID:2956093
 A:Accession: A27107
 A:Molecule type: Protein
 A:Residues: 1-318 <WEB>
 A:Experimental source: Intestinal epithelium
 A:Comment: Annexins undergo reversible, calcium-dependent binding to membrane phospholip
 detergent.

C:Superfamily: annexin I; annexin repeat homology
 C/Keywords: blocked amino end; calcium binding; duplication; endonexin fold; glycoprotein
 F:16-87/Domain: annexin repeat homology <AX1>
 F:27-43/Region: endonexin fold #status predicted
 F:88-159/Domain: annexin repeat homology <AX2>
 F:99-115/Region: endonexin fold #status predicted
 F:111-243/Domain: annexin repeat homology <AX3>
 F:163-189/Region: endonexin fold #status predicted
 F:248-318/Domain: annexin repeat homology <AX4>
 F:248-274/Region: endonexin fold #status predicted
 F:1/Modified site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted
 F:6/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted
 F:124/244/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 57.3%; Score 915; DB 1; Length 318;

Best Local Similarity 57.3%; Pred. No. 1.9e-52;
 Matches 180; Conservative 55; Mismatches 79; Indels 0; Gaps 0;

QY 5 GTVTDFSGFDGRADAEVLKRAMKGLTDEDSITLNTLARSNAQROIAEERKTLFGRLV 64
 DB 5 GTVKAASGFMAEDADQLTKRAMKGLTDEDAIINLAVRSTQOEIRAKYKTTIGRLM 64

QY 65 NDMKSELGKREKLIIVALKMPSRLYDAVELKNAKLGAGDEKVLTEIIASRPEELPAIK 124
 DB 66 DDLKSELGNEQVILGMMPTLVYDQELRRAMKAGDEGCLLEIIASRPEELIRIN 124
 QY 125 QAYEEYGSNLEDVVDGTSGYQRMVLVLLQANRDPDTAIDDAQVELDAQALFOAGELK 184
 DB 126 QTYOQYGRSLIEDDIRSTSPMFQRLVLSAGRDESNVLDALMQDAQDLVEAGEKK 185
 QY 185 WGTDEKFTITLIGRSVSHLRVDPKMTISGFOIEETIDRETSGNLENTLLAVKSI 244
 DB 186 WGTDEVKFLVLCSENRNHLHFDEYKRIAQKDIEQISKTSGSFEDALLAIVKCMRN 244
 QY 245 IPAYLAETLYYAMKAGTDHDLIRVVSSEIDLFNIRKPRKPFATSLYSMTIKGDTSG 304
 DB 246 KSAIFYAEELYSKMGKLTDDTLIRVVSRAEIMDLIRANKRLYKSLYSFIKGDTS 304
 QY 305 DYKXALLILCGED 318
 DB 306 DYKXVLLILCGED 318

RESULT 11

JC2029
 N:Annexin - chicken
 C/Species: Gallus gallus (chicken)
 C/Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 17-Mar-1999
 C/Accession: JC2029
 R:Caio, X.; Genge, B.R.; Wu, L.N.Y.; Buzzl, W.R.; Showman, R.M.; Wuthier, R.E.
 Biochem. Biophys. Res. Commun. 197, 556-561, 1993
 A:Title: Characterization, cloning and expression of the 67-kDa annexin from chicken
 A:Reference number: JC2029; MUID:94092130; PMID:8267590
 A:Accession: JC2029
 A:Molecule type: mRNA
 A:Residues: 1-671 <CAO>

C:Superfamily: annexin VI; annexin repeat homology
 C/Keywords: calcium binding; phospholipid binding
 F:21-92/Domain: annexin repeat homology <AX1>
 F:93-164/Domain: annexin repeat homology <AX2>
 F:176-248/Domain: annexin repeat homology <AX3>
 F:252-323/Domain: annexin repeat homology <AX4>
 F:364-435/Domain: annexin repeat homology <AX5>
 F:435-507/Domain: annexin repeat homology <AX6>
 F:525-597/Domain: annexin repeat homology <AX7>
 F:601-671/Domain: annexin repeat homology <AX8>

Query Match 56.2%; Score 898; DB 2; Length 671;
 Best Local Similarity 57.0%; Pred. No. 6.3e-51;
 Matches 180; Conservative 54; Mismatches 82; Indels 0; Gaps 0;

QY 4 RGTVTDFSGFDGRADAEVLKRAMKGLTDEDSITLNTLARSNAQROIAEERKTLFGRLV 63
 DB 9 RGSVDPDFEFNASQADALCNAMKGFSGDKDAIIDLTIRSNKORLEICAYXSQYKDL 68
 QY 64 NDMKSELGKREKLIIVALKMPSRLYDAVELKNAKLGAGDEKVLTEIIASRPEELPAIK 123
 DB 65 IADIKELTGKREKLIIVALKMPSRLYDAVELKNAKLGAGDEKVLTEIIASRPEELPAIK 128
 QY 124 QAYEEYGSNLEDVVDGTSGYQRMVLVLLQANRDPDTAIDDAQVELDAQALFOAGELK 183
 DB 125 VAAVYKAYRDLADVDVDTSGHFKKMLVLLQANREDDVVSDDLVEQAKDLLEAGEL 186
 QY 184 KNGTDEKFTITLIGRSVSHLRVDPKMTISGFOIEETIDRETSGNLENTLLAVKSI 243
 DB 189 KNGTDEKFTITLIGRSVSHLRVDPKMTISGFOIEETIDRETSGNLENTLLAVKSI 246
 QY 244 SIPAYLAETLYYAMKAGTDHDLIRVVSSEIDLFNIRKPRKPFATSLYSMTIKGDTSG 303
 DB 249 STAEFYAEELYSKMGKLTDDTLIRVVSRAEIMDLIRANKRLYKSLYSFIKGDTS 308
 QY 304 DYKXALLILCGED 319

Db 309 GEYKALLKLCESGDD 324

RESULT 12

LUB011

annexin XI - rabbit

N/Alternate names: calyculin-associated annexin protein CAP-50

C/Species: Oryctolagus cuniculus (domestic rabbit)

C/Date: 30-Sep-1993 #sequence revision 30-Sep-1993 #text_change 16-Jun-2000

C/Accession: J06094, F00501, A38250, P60263

R/Tokumitsu, H.; Mizutani, A.; Muramatsu, M.; Yokota, T.; Arai, K.; Hidaka, H.

Biochem. Biophys. Res. Commun. 186, 1227-1235, 1992

A/Title: Molecular cloning of rabbit CAP-50, a calyculin-associated annexin protein.

A/Reference number: J06094; MUID:92378579; PMID:1380798

A/Accession: J06094

A/Molecule type: mRNA

A/Residues: 1-503 <TK>

A/Cross-references: DBU:ID0883; NID:9471147; PID:BA01705.1; PID:9471148

A/Experimental source: lung

A/Accession: P00950

A/Molecule type: protein

A/Residues: 104-141/213-223, 'X', 225-231/254-263/270-280/285-309/319-337/429-448/478-492 <TK2>

R/Tokumitsu, H.; Mizutani, A.; Minami, H.; Kobayashi, R.; Hidaka, H.

J. Biol. Chem. 267, 8919-8924, 1992

A/Title: A calyculin-associated protein is a newly identified member of the Ca(2+)/phospho

A/Reference number: A38250; MUID:9250478; PMID:1533622

A/Accession: A38250

A/Molecule type: protein

A/Residues: 104-141/213-223, 'X', 225-231/254-263/270-280/285-291, 'X', 293-300, 'X', 302-309,

C/Comment: This protein binds specifically to calyculin in a Ca2+ dependent manner.

C/Keywords: calcium binding; annexin repeat homology

F/201-272/Domain: annexin repeat homology <AX1>

F/212-228/Region: endoneixin fold #status predicted

F/273-344/Domain: annexin repeat homology <AX2>

F/284-300/Region: endoneixin fold #status predicted

F/356-428/Domain: annexin repeat homology <AX3>

F/368-384/Region: endoneixin fold #status predicted

F/432-503/Domain: annexin repeat homology <AX4>

F/443-459/Region: endoneixin fold #status predicted

F/58/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match Best Local Similarity 54.8%; Score 876; DB 1; Length 503;

Matches 175; Conservative 56; Mismatches 84; Indels 0; Gaps 0;

```

QY 4 RGVTPDPSGFGDADAVLRAMKGLGTDSDSIINLLTARSNAHQOQIAEEFKTLFGRLD 63
DB 189 RGVTPDPSGFGDADAVLRAMKGLGTDSDSIINLLTARSNAHQOQIAEEFKTLFGRLD 248
QY 64 VDMKSELTKGPEKLIIVALKMPSRLYDAVELKHAAGAGTDEKVLTEIIASRTPEELRAI 123
DB 249 IVDLKSLSGNFEKTLILMKTPIVLPDAVEIKKAKAGTDEACILFIASRNEHIREL 308
QY 124 KQAYEEYGSNLEDDVVDTSYGYQRMVLVLLQANRDPDAIDDAQVELDAQALFQAGEL 183
DB 309 NRVYKTEFKTLEEARSDTSYGFQRLISLSQNRDSTNVMSTLVQDVQELVAAEIN 368
QY 184 KMGTDSEKFTIILGTRSVSHLRVPDKMTISGQIETIDRETSGLLELLAVYKSIIR 243
DB 369 FLGTDSEKFNVALICSRSPAHLVAVFNEYQRMGTGDIKSIKREMSGLDEQGLAVYKCIK 428
QY 244 SIPIYLAETLYYAMKAGTDHDLIRIVISRSSEIDLFINRKEFRKFNATSLYMIKGDTS 303
DB 429 NTPAFFAERLNKAMKAGTDRLLIRIMVSRSEIDLDIRAIVKMGKSLYHDISGDTIS 488
QY 304 GDYKALLLLCGGED 318
DB 489 GDYKILLKTCGGND 503

```

RESULT 13

LUB011

annexin XI form A - bovine

N/Alternate names: calyculin-associated protein peptide, CAP-50

C/Species: Bos primigenius taurus (cattle) #sequence revision 31-Mar-1993 #text_change 22-Jun-1999

C/Date: 31-Mar-1993 #sequence revision 31-Mar-1993 #text_change 22-Jun-1999

C/Accession: A42113; A42909; B42909; C42909; D42909

R/Towle, C.A.; Treadwell, B.V.

J. Biol. Chem. 267, 5416-5423, 1992

A/Title: Identification of a novel mammalian annexin. cDNA cloning, sequence analysis

A/Reference number: A42113; MUID:92184796; PMID:1372001

A/Accession: A42113

A/Molecule type: mRNA

A/Residues: 1-503 <TOW>

A/Cross-references: GB:M82802; NID:9162673; PID:AAA30379.1; PID:9162674

A/Note: the authors did not translate the codon GAC for residue 503

R/Mizutani, A.; Usuda, N.; Tokumitsu, H.; Minami, H.; Yasui, K.; Kobayashi, R.; Hidaka

J. Biol. Chem. 267, 13498-13504, 1992

A/Title: CAP-50, a newly identified annexin, localizes in nuclei of cultured fibroblasts

A/Reference number: A42909; MUID:92317074; PMID:1618851

A/Accession: A42909

A/Molecule type: protein

A/Residues: 213-223, 'X', 225-226/319-325, 'G', 327-328, 'X', 330-333, 'Q', 335-339/441-450, 'A'

A/Experimental source: lung

C/Comment: sequence modified after extraction from NCBI backbone

C/Note: Annexins undergo reversible, calcium-dependent binding to membrane phospholipids.

C/Genetics:

A/Introns: 19/1; 56/2

A/Note: the list of introns is incomplete

C/Superfamily: annexin VII; annexin repeat homology

C/Keywords: calcium binding; duplication; endoneixin fold; glycoprotein; phospholipid

F/201-272/Domain: annexin repeat homology <AX1>

F/212-228/Region: endoneixin fold #status predicted

F/273-344/Domain: annexin repeat homology <AX2>

F/284-300/Region: endoneixin fold #status predicted

F/356-428/Domain: annexin repeat homology <AX3>

F/368-384/Region: endoneixin fold #status predicted

F/432-503/Domain: annexin repeat homology <AX4>

F/443-459/Region: endoneixin fold #status predicted

F/59/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match Best Local Similarity 54.4%; Score 870; DB 1; Length 503;

Matches 175; Conservative 54; Mismatches 86; Indels 0; Gaps 0;

```

QY 4 RGVTPDPSGFGDADAVLRAMKGLGTDSDSIINLLTARSNAHQOQIAEEFKTLFGRLD 63
DB 189 RGVTPDPSGFGDADAVLRAMKGLGTDSDSIINLLTARSNAHQOQIAEEFKTLFGRLD 248
QY 64 VDMKSELTKGPEKLIIVALKMPSRLYDAVELKHAAGAGTDEKVLTEIIASRTPEELRAI 123
DB 249 IVDLKSLSGNFEKTLILMKTPIVLPDAVEIKKAKAGTDEACILFIASRNEHIREL 308
QY 124 KQAYEEYGSNLEDDVVDTSYGYQRMVLVLLQANRDPDAIDDAQVELDAQALFQAGEL 183
DB 309 NRVYKTEFKTLEEARSDTSYGFQRLISLSQNRDSTNVMSTLVQDVQELVAAEIN 368
QY 184 KMGTDSEKFTIILGTRSVSHLRVPDKMTISGQIETIDRETSGLLELLAVYKSIIR 243
DB 369 FLGTDSEKFNVALICSRSPAHLVAVFNEYQRMGTGDIKSIKREMSGLDEQGLAVYKCIK 428
QY 244 SIPIYLAETLYYAMKAGTDHDLIRIVISRSSEIDLFINRKEFRKFNATSLYMIKGDTS 303
DB 429 NTPAFFAERLNKAMKAGTDRLLIRIMVSRSEIDLDIRAIVKMGKSLYHDISGDTIS 488
QY 304 GDYKALLLLCGGED 318
DB 489 GDYKILLKTCGGND 503

```

RESULT 14

S23447

annexin XI form B - bovine

C/Species: Bos primigenius taurus (cattle)

C/Date: 22-Nov-1993 #sequence_revision 10-Feb-1995 #text_change 22-Jun-1999
 C/Accession: S23447; S36136
 R/Towle, C.
 submitted to the EMBL Data Library, February 1992
 A/Reference number: S23447
 A/Accession: S23447
 A/Molecule type: mRNA
 A/Residues: 1-505 <TOM>
 A/Cross-references: EMBL:Z11742; NID:g77; PIDN:CAA7801.1; PID:g78
 R/Towle, C.A.; Weisbach, L.; Treadwell, B.V.
 Biochim. Biophys. Acta 1131, 223-226, 1992
 A/Title: Alternatively spliced annexin XI transcripts encode proteins that differ near
 A/Reference number: S36136; MUID:92305067; PMID:1535225
 A/Accession: S36136
 A/Molecule type: mRNA
 A/Residues: 1-77 <TOM>
 A/Cross-references: EMBL:Z11742
 C/Comment: Annexins undergo reversible, calcium-dependent binding to membrane phospholipid
 deriscod.
 C/Genetics:
 A/Introns: 19/1; 58/2
 A/Note: the list of introns is incomplete
 C/Superfamily: annexin VII; annexin repeat homology
 C/Keywords: alternative splicing; calcium binding; duplication; endonexin fold; glycoproc
 F:203-274/Domain: annexin repeat homology <AX1>
 F:214-230/Domain: endonexin fold #status predicted
 F:275-346/Domain: annexin repeat homology <AX2>
 F:286-302/Region: endonexin fold #status predicted
 F:358-430/Domain: annexin repeat homology <AX3>
 F:370-386/Region: endonexin fold #status predicted
 F:434-505/Domain: annexin repeat homology <AX4>
 F:445-461/Region: endonexin fold #status predicted
 F:61.113/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 54.4%; Score 870; DB 1; Length 505;
 Best Local Similarity 55.6%; Pred. No. 2.9e-49;
 Matches 175; Conservative 54; Mismatches 86; Indels 0; Gaps 0;

Qy 4 RGVTVDFSGFDGRADAEVLRKAMKGLTDEDSITLNTLRASNAQRQIAEEFKTLFGRL 63
 Db 191 RGTITDAPGFDPLRDAEVLRRAMKGFDEQAIIIDCLSSRNKQOQIILSKTYAGDL 250
 Qy 64 VNDKSELTKGFEKLIYALMKPSRLYDAVEILKAKLGAGTDEKVLTEIIASRPEELRAI 123
 Db 251 IKDLSKSELGNFEKTLIYALMKTPVLPDAVEIKKAIKAGTDEACILIELIASSNHIREL 310
 Qy 124 KQAYEEYGSNIEDDVVGDTSGYQRMVLVLLQANRDPDPAIDDAQVELDAQALFQAGEL 183
 Db 311 NRVYKTFPKKTLBEAIRSDTSGHFORLLISLQGNRDESTVMDTLVQRDVDELTAAGEN 370
 Qy 184 KMGTDSEKFTITLIGRSVSHLRVDPKYMISGFOIETIDRETSGNLENLLAVVKSIR 243
 Db 371 RLGTDESKFNALICSRRAHLVAVFNQYQMTGRDIEKICREMSGDLQGMVLAVKCLK 430
 Qy 244 SIPYLAETLYYAMKAGTDDTLIRIVYSRSEIDLFNIRKEFRKNFATSLYSYIKGDT 303
 Db 431 NTPAFPAERLNKARAGAGTDRTLIRIVWSRSEIDLIRAEYKRLYKGLYHDTGDS 490
 Qy 304 GDYKRLLLCGGED 318
 Db 491 GDYKRLLLCGGND 505

RESULT 15
 A53152
 annexin XI - human
 C/Species: Homo sapiens (man)
 C/Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 13-Aug-1999
 C/Accession: A53152
 R/Misaki, Y.; Pruijn, G.J.N.; van der Kemp, A.W.C.M.; van Venrooij, W.J.
 J. Biol. Chem. 269, 4240-4246, 1994
 A/Title: The 56k autoantigen is identical to human annexin XI.
 A/Reference number: A53152; MUID:94140847; PMID:7508441

A/Accession: A53152
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-505 <MIS>
 A/Cross-references: GB:LL9605; NID:g457128; PIDN:AAA19734.1; PID:g457129
 C/Genetics:
 A/Gene: GDB:ANX11
 A/Map position: GDB:313076
 A/Cross-references: GDB:313076
 A/Map position: 9q11-9q22
 C/Superfamily: annexin VII; annexin repeat homology
 C/Keywords: calcium binding; duplication; endonexin fold; glycoprotein; phospholipid
 F:203-274/Domain: annexin repeat homology <AX1>
 F:275-346/Domain: annexin repeat homology <AX2>
 F:358-430/Domain: annexin repeat homology <AX3>
 F:434-505/Domain: annexin repeat homology <AX4>

Query Match 53.7%; Score 858; DB 2; Length 505;
 Best Local Similarity 54.3%; Pred. No. 1.8e-48;
 Matches 171; Conservative 56; Mismatches 88; Indels 0; Gaps 0;

Qy 4 RGVTVDFSGFDGRADAEVLRKAMKGLTDEDSITLNTLRASNAQRQIAEEFKTLFGRL 63
 Db 191 RGTITDAPGFDPLRDAEVLRRAMKGFDEQAIIIDCLSSRNKQOQIILSKTYAGDL 250
 Qy 64 VNDKSELTKGFEKLIYALMKPSRLYDAVEILKAKLGAGTDEKVLTEIIASRPEELRAI 123
 Db 251 IKDLSKSELGNFEKTLIYALMKTPVLPDAVEIKKAIKAGTDEACILIELIASSNHIREL 310
 Qy 124 KQAYEEYGSNIEDDVVGDTSGYQRMVLVLLQANRDPDPAIDDAQVELDAQALFQAGEL 183
 Db 311 NRVYKTFPKKTLBEAIRSDTSGHFORLLISLQGNRDESTVMDTLVQRDVDELTAAGEN 370
 Qy 184 KMGTDSEKFTITLIGRSVSHLRVDPKYMISGFOIETIDRETSGNLENLLAVVKSIR 243
 Db 371 RLGTDESKFNALICSRRAHLVAVFNQYQMTGRDIEKICREMSGDLQGMVLAVKCLK 430
 Qy 244 SIPYLAETLYYAMKAGTDDTLIRIVYSRSEIDLFNIRKEFRKNFATSLYSYIKGDT 303
 Db 431 NTPAFPAERLNKARAGAGTDRTLIRIVWSRSEIDLIRAEYKRLYKGLYHDTGDS 490
 Qy 304 GDYKRLLLCGGED 318
 Db 491 GDYKRLLLCGGND 505

Search completed: December 12, 2003, 14:52:40
 Job time: 11.6549 secs